

1/233

SEQUENCE LISTING

<110> Sagami Chemical Research Center,
Protegene Inc.

<120> Human proteins having hydrophobic domains and DNAs encoding these
proteins

<130> 661607

<150> JP 10-326255

<151> 1998-11-17

<150> JP 10-364315

<151> 1998-12-22

<150> JP 11-69811

<151> 1999-03-16

<150> JP 11-119299

<151> 1999-04-27

<150> JP 11-138169

<151> 1999-05-19

<160> 150

<210> 1

<211> 647

<212> PRT

<213> Homo sapiens

<400> 1

Met Ala Glu Glu Glu Ala Pro Lys Lys Ser Arg Ala Ala Gly Gly Gly

1

5

10

15

Ala Ser Trp Glu Leu Cys Ala Gly Ala Leu Ser Ala Arg Leu Thr Glu

2/233

	20		25		30
Glu Gly Ser Gly Asp Ala Gly Gly Arg Arg Arg Pro Pro Val Asp Pro					
35		40		45	
Arg Arg Leu Ala Arg Gln Leu Leu Leu Leu Trp Leu Leu Glu Ala					
50		55		60	
Pro Leu Leu Leu Gly Val Arg Ala Gln Ala Ala Gly Gln Gly Pro Gly					
65		70		75	80
Gln Gly Pro Gly Pro Gly Gln Gln Pro Pro Pro Pro Pro Gln Gln Gln					
85		90		95	
Gln Ser Gly Gln Gln Tyr Asn Gly Glu Arg Gly Ile Ser Val Pro Asp					
100		105		110	
His Gly Tyr Cys Gln Pro Ile Ser Ile Pro Leu Cys Thr Asp Ile Ala					
115		120		125	
Tyr Asn Gln Thr Ile Met Pro Asn Leu Leu Gly His Thr Asn Gln Glu					
130		135		140	
Asp Ala Gly Leu Glu Val His Gln Phe Tyr Pro Leu Val Lys Val Gln					
145		150		155	160
Cys Ser Ala Glu Leu Lys Phe Phe Leu Cys Ser Met Tyr Ala Pro Val					
165		170		175	
Cys Thr Val Leu Glu Gln Ala Leu Pro Pro Cys Arg Ser Leu Cys Glu					
180		185		190	
Arg Ala Arg Gln Gly Cys Glu Ala Leu Met Asn Lys Phe Gly Phe Gln					
195		200		205	
Trp Pro Asp Thr Leu Lys Cys Glu Lys Phe Pro Val His Gly Ala Gly					
210		215		220	
Glu Leu Cys Val Gly Gln Asn Thr Ser Asp Lys Gly Thr Pro Thr Pro					
225		230		235	240
Ser Leu Leu Pro Glu Phe Trp Thr Ser Asn Pro Gln His Gly Gly Gly					
245		250		255	
Gly His Arg Gly Gly Phe Pro Gly Gly Ala Gly Ala Ser Glu Arg Gly					
260		265		270	
Lys Phe Ser Cys Pro Arg Ala Leu Lys Val Pro Ser Tyr Leu Asn Tyr					
275		280		285	
His Phe Leu Gly Glu Lys Asp Cys Gly Ala Pro Cys Glu Pro Thr Lys					
290		295		300	

3/233

Val Tyr Gly Leu Met Tyr Phe Gly Pro Glu Glu Leu Arg Phe Ser Arg
 305 310 315 320
 Thr Trp Ile Gly Ile Trp Ser Val Leu Cys Cys Ala Ser Thr Leu Phe
 325 330 335
 Thr Val Leu Thr Tyr Leu Val Asp Met Arg Arg Phe Ser Tyr Pro Glu
 340 345 350
 Arg Pro Ile Ile Phe Leu Ser Gly Cys Tyr Thr Ala Val Ala Val Ala
 355 360 365
 Tyr Ile Ala Gly Phe Leu Leu Glu Asp Arg Val Val Cys Asn Asp Lys
 370 375 380
 Phe Ala Glu Asp Gly Ala Arg Thr Val Ala Gln Gly Thr Lys Lys Glu
 385 390 395 400
 Gly Cys Thr Ile Leu Phe Met Met Leu Tyr Phe Phe Ser Met Ala Ser
 405 410 415
 Ser Ile Trp Trp Val Ile Leu Ser Leu Thr Trp Phe Leu Ala Ala Gly
 420 425 430
 Met Lys Trp Gly His Glu Ala Ile Glu Ala Asn Ser Gln Tyr Phe His
 435 440 445
 Leu Ala Ala Trp Ala Val Pro Ala Ile Lys Thr Ile Thr Ile Leu Ala
 450 455 460
 Leu Gly Gln Val Asp Gly Asp Val Leu Ser Gly Val Cys Phe Val Gly
 465 470 475 480
 Leu Asn Asn Val Asp Ala Leu Arg Gly Phe Val Leu Ala Pro Leu Phe
 485 490 495
 Val Tyr Leu Phe Ile Gly Thr Ser Phe Leu Leu Ala Gly Phe Val Ser
 500 505 510
 Leu Phe Arg Ile Arg Thr Ile Met Lys His Asp Gly Thr Lys Thr Glu
 515 520 525
 Lys Leu Glu Lys Leu Met Val Arg Ile Gly Val Phe Ser Val Leu Tyr
 530 535 540
 Thr Val Pro Ala Thr Ile Val Ile Ala Cys Tyr Phe Tyr Glu Gln Ala
 545 550 555 560
 Phe Arg Asp Gln Trp Glu Arg Ser Trp Val Ala Gln Ser Cys Lys Ser
 565 570 575
 Tyr Ala Ile Pro Cys Pro His Leu Gln Ala Gly Gly Gly Ala Pro Pro

4/233

580	585	590
His Pro Pro Met Ser Pro Asp Phe Thr Val Phe Met Ile Lys Tyr Leu		
595	600	605
Met Thr Leu Ile Val Gly Ile Thr Ser Gly Phe Trp Ile Trp Ser Gly		
610	615	620
Lys Thr Leu Asn Ser Trp Arg Lys Phe Tyr Thr Arg Leu Thr Asn Ser		
625	630	635
Lys Gln Gly Glu Thr Thr Val		640
645		

<210> 2

<211> 350

<212> PRT

<213> Homo sapiens

<400> 2

Met His Pro Ala Ala Phe Pro Leu Pro Val Val Val Ala Ala Val Leu			
1	5	10	15
Trp Gly Ala Ala Pro Thr Arg Gly Leu Ile Arg Ala Thr Ser Asp His			
20	25	30	
Asn Ala Ser Met Asp Phe Ala Asp Leu Pro Ala Leu Phe Gly Ala Thr			
35	40	45	
Leu Ser Gln Glu Gly Leu Gln Gly Phe Leu Val Glu Ala His Pro Asp			
50	55	60	
Asn Ala Cys Ser Pro Ile Ala Pro Pro Pro Pro Ala Pro Val Asn Gly			
65	70	75	80
Ser Val Phe Ile Ala Leu Leu Arg Arg Phe Asp Cys Asn Phe Asp Leu			
85	90	95	
Lys Val Leu Asn Ala Gln Lys Ala Gly Tyr Gly Ala Ala Val Val His			
100	105	110	
Asn Val Asn Ser Asn Glu Leu Leu Asn Met Val Trp Asn Ser Glu Glu			
115	120	125	
Ile Gln Gln Gln Ile Trp Ile Pro Ser Val Phe Ile Gly Glu Arg Ser			
130	135	140	
Ser Glu Tyr Leu Arg Ala Leu Phe Val Tyr Glu Lys Gly Ala Arg Val			
145	150	155	160

5/233

Leu Leu Val Pro Asp Asn Thr Phe Pro Leu Gly Tyr Tyr Leu Ile Pro
 165 170 175
 Phe Thr Gly Ile Val Gly Leu Leu Val Leu Ala Met Gly Ala Val Met
 180 185 190
 Ile Ala Arg Cys Ile Gln His Arg Lys Arg Leu Gln Arg Asn Arg Leu
 195 200 205
 Thr Lys Glu Gln Leu Lys Gln Ile Pro Thr His Asp Tyr Gln Lys Gly
 210 215 220
 Asp Gln Tyr Asp Val Cys Ala Ile Cys Leu Asp Glu Tyr Glu Asp Gly
 225 230 235 240
 Asp Lys Leu Arg Val Leu Pro Cys Ala His Ala Tyr His Ser Arg Cys
 245 250 255
 Val Asp Pro Trp Leu Thr Gln Thr Arg Lys Thr Cys Pro Ile Cys Lys
 260 265 270
 Gln Pro Val His Arg Gly Pro Gly Asp Glu Asp Gln Glu Glu Glu Thr
 275 280 285
 Gln Gly Gln Glu Glu Gly Asp Glu Gly Glu Pro Arg Asp His Pro Ala
 290 295 300
 Ser Glu Arg Thr Pro Leu Leu Gly Ser Ser Pro Thr Leu Pro Thr Ser
 305 310 315 320
 Phe Gly Ser Leu Ala Pro Ala Pro Leu Val Phe Pro Gly Pro Ser Thr
 325 330 335
 Asp Pro Pro Leu Ser Pro Pro Ser Ser Pro Val Ile Leu Val
 340 345 350

<210> 3

<211> 206

<212> PRT

<213> Homo sapiens

<400> 3

Met Gly Leu Gly Gln Pro Gln Ala Trp Leu Leu Gly Leu Pro Thr Ala
 1 5 10 15
 Val Val Tyr Gly Ser Leu Ala Leu Phe Thr Thr Ile Leu His Asn Val
 20 25 30
 Phe Leu Leu Tyr Tyr Val Asp Thr Phe Val Ser Val Tyr Lys Ile Asn

6/233

35	40	45
Lys Met Ala Phe Trp Val Gly Glu Thr Val Phe Leu Leu Trp Asn Ser		
50	55	60
Leu Asn Asp Pro Leu Phe Gly Trp Leu Ser Asp Arg Gln Phe Leu Ser		
65	70	75
Ser Gln Pro Arg Gly Arg Asp Leu Pro Trp Leu Gly Leu Val Gly Pro		
85	90	95
Ser Gly Leu Trp Thr Ala Asn Thr Leu Cys Cys Phe Trp Lys Ile Pro		
100	105	110
Leu Pro His Pro Cys Leu Ser Pro Ser Ser Pro Pro Thr Leu Arg Ser		
115	120	125
Gly His Pro Ile Pro Phe Gly His Gln Pro Asn Arg Leu Ile Arg Gly		
130	135	140
Trp Lys Leu Gly Gln Arg Arg Arg Val Tyr Pro Leu Val Arg Arg Arg		
145	150	155
Ala Leu Leu Lys Gly Cys Gly Ala Gly Pro Gly Ala Gly Pro Gly Leu		
165	170	175
Ala Trp Ala Ala Ala Gly Ala Val Val Pro Gly Val Leu Gly Ala Leu		
180	185	190
Gly Pro Ser Trp Pro Ala Val Leu Ala Val Pro Val Pro Leu		
195	200	205

<210> 4

<211> 213

<212> PRT

<213> Homo sapiens

<400> 4

Met His Tyr Tyr Arg Tyr Ser Asn Ala Lys Val Ser Cys Trp Tyr Lys		
1	5	10
Tyr Leu Leu Phe Ser Tyr Asn Ile Ile Phe Trp Leu Ala Gly Val Val		
20	25	30
Phe Leu Gly Val Gly Leu Trp Ala Trp Ser Glu Lys Gly Val Leu Ser		
35	40	45
Asp Leu Thr Lys Val Thr Arg Met His Gly Ile Asp Pro Val Val Leu		
50	55	60

7/233

Val Leu Met Val Gly Val Val Met Phe Thr Leu Gly Phe Ala Gly Cys
 65 70 75 80
 Val Gly Ala Leu Arg Glu Asn Ile Cys Leu Leu Asn Phe Asn Gln Cys
 85 90 95
 Cys Gly Ala Tyr Gly Pro Glu Asp Trp Asp Leu Asn Val Tyr Phe Asn
 100 105 110
 Cys Ser Gly Ala Ser Tyr Ser Arg Glu Lys Cys Gly Val Pro Phe Ser
 115 120 125
 Cys Cys Val Pro Asp Pro Ala Gln Lys Val Val Asn Thr Gln Cys Gly
 130 135 140
 Tyr Asp Val Arg Ile Gln Leu Lys Ser Lys Trp Asp Glu Ser Ile Phe
 145 150 155 160
 Thr Lys Gly Cys Ile Gln Ala Leu Glu Ser Trp Leu Pro Arg Asn Ile
 165 170 175
 Tyr Ile Val Ala Gly Val Phe Ile Ala Ile Ser Leu Leu Gln Ile Phe
 180 185 190
 Gly Ile Phe Leu Ala Arg Thr Leu Ile Ser Asp Ile Glu Ala Val Lys
 195 200 205
 Ala Gly His His Phe
 210

<210> 5

<211> 595

<212> PRT

<213> Homo sapiens

<400> 5

Met Arg Ala Ala Arg Ala Ala Pro Leu Leu Gln Leu Leu Leu Leu
 1 5 10 15
 Gly Pro Trp Leu Glu Ala Ala Gly Val Ala Glu Ser Pro Leu Pro Ala
 20 25 30
 Val Val Leu Ala Ile Leu Ala Arg Asn Ala Glu His Ser Leu Pro His
 35 40 45
 Tyr Leu Gly Ala Leu Glu Arg Leu Asp Tyr Pro Arg Ala Arg Met Ala
 50 55 60
 Leu Trp Cys Ala Thr Asp His Asn Val Asp Asn Thr Thr Glu Met Leu

8/233

65	70	75	80
Gln Glu Trp Leu Ala Ala Val Gly Asp Asp Tyr Ala Ala Val Val Trp			
85	90	95	
Arg Pro Glu Gly Glu Pro Arg Phe Tyr Pro Asp Glu Glu Gly Pro Lys			
100	105	110	
His Trp Thr Lys Glu Arg His Gln Phe Leu Met Glu Leu Lys Gln Glu			
115	120	125	
Ala Leu Thr Phe Ala Arg Asn Trp Gly Ala Asp Tyr Ile Leu Phe Ala			
130	135	140	
Asp Thr Asp Asn Ile Leu Thr Asn Asn Gln Thr Leu Arg Leu Leu Met			
145	150	155	160
Gly Gln Gly Leu Pro Val Val Ala Pro Met Leu Asp Ser Gln Thr Tyr			
165	170	175	
Tyr Ser Asn Phe Trp Cys Gly Ile Thr Pro Gln Gly Tyr Tyr Arg Arg			
180	185	190	
Thr Ala Glu Tyr Phe Pro Thr Lys Asn Arg Gln Arg Arg Gly Cys Phe			
195	200	205	
Arg Val Pro Met Val His Ser Thr Phe Leu Ala Ser Leu Arg Ala Glu			
210	215	220	
Gly Ala Asp Gln Leu Ala Phe Tyr Pro Pro His Pro Asn Tyr Thr Trp			
225	230	235	240
Pro Phe Asp Asp Ile Ile Val Phe Ala Tyr Ala Cys Gln Ala Ala Gly			
245	250	255	
Val Ser Val His Val Cys Asn Glu His Arg Tyr Gly Tyr Met Asn Val			
260	265	270	
Pro Val Lys Ser His Gln Gly Leu Glu Asp Glu Arg Val Asn Phe Ile			
275	280	285	
His Leu Ile Leu Glu Ala Leu Val Asp Gly Pro Arg Met Gln Ala Ser			
290	295	300	
Ala His Val Thr Arg Pro Ser Lys Arg Pro Ser Lys Ile Gly Phe Asp			
305	310	315	320
Glu Val Phe Val Ile Ser Leu Ala Arg Arg Pro Asp Arg Arg Glu Arg			
325	330	335	
Met Leu Ala Ser Leu Trp Glu Met Glu Ile Ser Gly Arg Val Val Asp			
340	345	350	

9/233

Ala Val Asp Gly Trp Met Leu Asn Ser Ser Ala Ile Arg Asn Leu Gly
 355 360 365
 Val Asp Leu Leu Pro Gly Tyr Gln Asp Pro Tyr Ser Gly Arg Thr Leu
 370 375 380
 Thr Lys Gly Glu Val Gly Cys Phe Leu Ser His Tyr Ser Ile Trp Glu
 385 390 395 400
 Glu Val Val Ala Arg Gly Leu Ala Arg Val Leu Val Phe Glu Asp Asp
 405 410 415
 Val Arg Phe Glu Ser Asn Phe Arg Gly Arg Leu Glu Arg Leu Met Glu
 420 425 430
 Asp Val Glu Ala Glu Lys Leu Ser Trp Asp Leu Ile Tyr Leu Gly Arg
 435 440 445
 Lys Gln Val Asn Pro Glu Lys Glu Thr Ala Val Glu Gly Leu Pro Gly
 450 455 460
 Leu Val Val Ala Gly Tyr Ser Tyr Trp Thr Leu Ala Tyr Ala Leu Arg
 465 470 475 480
 Leu Ala Gly Ala Arg Lys Leu Leu Ala Ser Gln Pro Leu Arg Arg Met
 485 490 495
 Leu Pro Val Asp Glu Phe Leu Pro Ile Met Phe Asp Gln His Pro Asn
 500 505 510
 Glu Gln Tyr Lys Ala His Phe Trp Pro Arg Asp Leu Val Ala Phe Ser
 515 520 525
 Ala Gln Pro Leu Leu Ala Ala Pro Thr His Tyr Ala Gly Asp Ala Glu
 530 535 540
 Trp Leu Ser Asp Thr Glu Thr Ser Ser Pro Trp Asp Asp Asp Ser Gly
 545 550 555 560
 Arg Leu Ile Ser Trp Ser Gly Ser Gln Lys Thr Leu Arg Ser Pro Arg
 565 570 575
 Leu Asp Leu Thr Gly Ser Ser Gly His Ser Leu Gln Pro Gln Pro Arg
 580 585 590
 Asp Glu Leu
 595

<210> 6

<211> 264

10/233

<212> PRT

<213> Homo sapiens

<400> 6

Met Val Ala Ser Ala Lys Met Gly Arg Ala Gly Thr Met Ala Val Ala
1 5 10 15
Ala Glu Leu Arg Glu Leu Cys Pro Gly Val Asn Asn Gln Pro Tyr Leu
20 25 30
Cys Glu Ser Gly His Cys Cys Gly Glu Thr Gly Cys Cys Thr Tyr Tyr
35 40 45
Tyr Glu Leu Trp Trp Phe Trp Leu Leu Trp Thr Val Leu Ile Leu Phe
50 55 60
Ser Cys Cys Cys Ala Phe Arg His Arg Arg Ala Lys Leu Arg Leu Gln
65 70 75 80
Gln Gln Gln Arg Gln Arg Glu Ile Asn Leu Leu Ala Tyr His Gly Ala
85 90 95
Cys His Gly Ala Gly Pro Phe Pro Thr Gly Ser Leu Leu Asp Leu Arg
100 105 110
Phe Leu Ser Thr Phe Lys Pro Pro Ala Tyr Glu Asp Val Val His Arg
115 120 125
Pro Gly Thr Pro Pro Pro Pro Tyr Thr Val Ala Pro Gly Arg Pro Leu
130 135 140
Thr Ala Ser Ser Glu Gln Thr Cys Cys Ser Ser Ser Ser Ser Cys Pro
145 150 155 160
Ala His Phe Glu Gly Thr Asn Val Glu Gly Val Ser Ser His Gln Ser
165 170 175
Ala Pro Pro His Gln Glu Gly Glu Pro Gly Ala Gly Val Thr Pro Ala
180 185 190
Ser Thr Pro Pro Ser Cys Arg Tyr Arg Arg Leu Thr Gly Asp Ser Gly
195 200 205
Ile Glu Leu Cys Pro Cys Pro Ala Ser Gly Glu Gly Glu Pro Val Lys
210 215 220
Glu Val Arg Val Ser Ala Thr Leu Pro Asp Leu Glu Asp Tyr Ser Pro
225 230 235 240
Cys Ala Leu Pro Pro Glu Ser Val Pro Gln Ile Phe Pro Met Gly Leu
245 250 255

11/233

Ser Ser Ser Glu Gly Asp Ile Pro

260

<210> 7

<211> 343

<212> PRT

<213> Homo sapiens

<400> 7

Met Gln Pro Pro Pro Pro Gly Pro Leu Gly Asp Cys Leu Arg Asp Trp

1

5

10

15

Glu Asp Leu Gln Gln Asp Phe Gln Asn Ile Gln Glu Thr His Arg Leu

20

25

30

Tyr Arg Leu Lys Leu Glu Glu Leu Thr Lys Leu Gln Asn Asn Cys Thr

35

40

45

Ser Ser Ile Thr Arg Gln Lys Lys Arg Leu Gln Glu Leu Ala Leu Ala

50

55

60

Leu Lys Lys Cys Lys Pro Ser Leu Pro Ala Glu Ala Glu Gly Ala Ala

65

70

75

80

Gln Glu Leu Glu Asn Gln Met Lys Glu Arg Gln Gly Leu Phe Phe Asp

85

90

95

Met Glu Ala Tyr Leu Pro Lys Lys Asn Gly Leu Tyr Leu Ser Leu Val

100

105

110

Leu Gly Asn Val Asn Val Thr Leu Leu Ser Lys Gln Ala Lys Phe Ala

115

120

125

Tyr Lys Asp Glu Tyr Glu Lys Phe Lys Leu Tyr Leu Thr Ile Ile Leu

130

135

140

Ile Leu Ile Ser Phe Thr Cys Arg Phe Leu Leu Asn Ser Arg Val Thr

145

150

155

160

Asp Ala Ala Phe Asn Phe Leu Leu Val Trp Tyr Tyr Cys Thr Leu Thr

165

170

175

Ile Arg Glu Ser Ile Leu Ile Asn Asn Gly Ser Arg Ile Lys Gly Trp

180

185

190

Trp Val Phe His His Tyr Val Ser Thr Phe Leu Ser Gly Val Met Leu

195

200

205

Thr Trp Pro Asp Gly Leu Met Tyr Gln Lys Phe Arg Asn Gln Phe Leu

12/233

210	215	220
Ser Phe Ser Met Tyr Gln Ser Phe Val Gln Phe Leu Gln Tyr Tyr Tyr		
225	230	235 240
Gln Ser Gly Cys Leu Tyr Arg Leu Arg Ala Leu Gly Glu Arg His Thr		
245	250	255
Met Asp Leu Thr Val Glu Gly Phe Gln Ser Trp Met Trp Arg Gly Leu		
260	265	270
Thr Phe Leu Leu Pro Phe Leu Phe Phe Gly His Phe Trp Gln Leu Phe		
275	280	285
Asn Ala Leu Thr Leu Phe Asn Leu Ala Gln Asp Pro Gln Cys Lys Glu		
290	295	300
Trp Gln Val Leu Met Cys Gly Phe Pro Phe Leu Leu Leu Phe Leu Gly		
305	310	315 320
Asn Phe Phe Thr Thr Leu Arg Val Val His His Lys Phe His Ser Gln		
325	330	335
Arg His Gly Ser Lys Lys Asp		
340		

<210> 8

<211> 244

<212> PRT

<213> Homo sapiens

<400> 8

Met Asp Ile Leu Val Pro Leu Leu Gln Leu Leu Val Leu Leu Leu Thr		
1	5	10 15
Leu Pro Leu His Leu Met Ala Leu Leu Gly Cys Trp Gln Pro Leu Cys		
20	25	30
Lys Ser Tyr Phe Pro Tyr Leu Met Ala Val Leu Thr Pro Lys Ser Asn		
35	40	45
Arg Lys Met Glu Ser Lys Lys Arg Glu Leu Phe Ser Gln Ile Lys Gly		
50	55	60
Leu Thr Gly Ala Ser Gly Lys Val Ala Leu Leu Glu Leu Gly Cys Gly		
65	70	75 80
Thr Gly Ala Asn Phe Gln Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys		
85	90	95

13/233

Leu Asp Pro Asn Pro His Phe Glu Lys Phe Leu Thr Lys Ser Met Ala
 100 105 110
 Glu Asn Arg His Leu Gln Tyr Glu Arg Phe Val Val Ala Pro Gly Glu
 115 120 125
 Asp Met Arg Gln Leu Ala Asp Gly Ser Met Asp Val Val Val Cys Thr
 130 135 140
 Leu Val Leu Cys Ser Val Gln Ser Pro Arg Lys Val Leu Gln Glu Val
 145 150 155 160
 Arg Arg Val Leu Arg Pro Gly Gly Val Leu Phe Phe Trp Glu His Val
 165 170 175
 Ala Glu Pro Tyr Gly Ser Trp Ala Phe Met Trp Gln Gln Val Phe Glu
 180 185 190
 Pro Thr Trp Lys His Ile Gly Asp Gly Cys Cys Leu Thr Arg Glu Thr
 195 200 205
 Trp Lys Asp Leu Glu Asn Ala Gln Phe Ser Glu Ile Gln Met Glu Arg
 210 215 220
 Gln Pro Pro Pro Leu Lys Trp Leu Pro Val Gly Pro His Ile Met Gly
 225 230 235 240
 Lys Ala Val Lys

<210> 9

<211> 303

<212> PRT

<213> Homo sapiens

<400> 9

Met Lys Leu Lys Leu Lys Asn Val Phe Leu Ala Tyr Phe Leu Val Ser
 1 5 10 15
 Ile Ala Gly Leu Leu Tyr Ala Leu Val Gln Leu Gly Gln Pro Cys Asp
 20 25 30
 Cys Leu Pro Pro Leu Arg Ala Ala Ala Glu Gln Leu Arg Gln Lys Asp
 35 40 45
 Leu Arg Ile Ser Gln Leu Gln Ala Glu Leu Arg Arg Pro Pro Pro Ala
 50 55 60
 Pro Ala Gln Pro Pro Glu Pro Glu Ala Leu Pro Thr Ile Tyr Val Val

14/233

65	70	75	80
Thr Pro Thr Tyr Ala Arg Pro Leu Trp Val Gln Tyr Pro Gln Asp Val			
85	90	95	
Thr Thr Phe Asn Ile Asp Asp Gln Tyr Leu Leu Gly Asp Ala Leu Leu			
100	105	110	
Val His Pro Val Ser Asp Ser Gly Ala His Gly Val Gln Val Tyr Leu			
115	120	125	
Pro Gly Gln Gly Glu Val Trp Tyr Asp Ile Gln Ser Tyr Gln Lys His			
130	135	140	
His Gly Pro Gln Thr Leu Tyr Leu Pro Val Thr Leu Ser Ser Ile Pro			
145	150	155	160
Val Phe Gln Arg Gly Gly Thr Ile Val Pro Arg Trp Met Arg Val Arg			
165	170	175	
Arg Ser Ser Glu Cys Met Lys Asp Asp Pro Ile Thr Leu Phe Val Ala			
180	185	190	
Leu Ser Pro Gln Gly Thr Ala Gln Gly Glu Leu Phe Leu Asp Asp Gly			
195	200	205	
His Thr Phe Asn Tyr Gln Thr Arg Gln Glu Phe Leu Leu Arg Arg Phe			
210	215	220	
Ser Phe Ser Gly Asn Thr Leu Val Ser Ser Ser Ala Asp Pro Glu Gly			
225	230	235	240
His Phe Glu Thr Pro Ile Trp Ile Glu Arg Val Val Ile Ile Gly Ala			
245	250	255	
Gly Lys Pro Ala Ala Val Val Leu Gln Thr Lys Gly Ser Pro Glu Ser			
260	265	270	
Arg Leu Ser Phe Gln His Asp Pro Glu Thr Ser Val Leu Val Leu Arg			
275	280	285	
Lys Pro Gly Ile Asn Val Ala Ser Asp Trp Ser Ile His Leu Arg			
290	295	300	

<210> 10

<211> 160

<212> PRT

<213> Homo sapiens

<400> 10

15/233

Met Asp Lys Leu Lys Lys Val Leu Ser Gly Gln Asp Thr Glu Asp Arg
 1 5 10 15
 Ser Gly Leu Ser Glu Val Val Glu Ala Ser Ser Leu Ser Trp Ser Thr
 20 25 30
 Arg Ile Lys Gly Phe Ile Ala Cys Phe Ala Ile Gly Ile Leu Cys Ser
 35 40 45
 Leu Leu Gly Thr Val Leu Leu Trp Val Pro Arg Lys Gly Leu His Leu
 50 55 60
 Phe Ala Val Phe Tyr Thr Phe Gly Asn Ile Ala Ser Ile Gly Ser Thr
 65 70 75 80
 Ile Phe Leu Met Gly Pro Val Lys Gln Leu Lys Arg Met Phe Glu Pro
 85 90 95
 Thr Arg Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe Ala Leu Thr
 100 105 110
 Leu Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala Leu Ile Phe
 115 120 125
 Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu Ser Phe Ile
 130 135 140
 Pro Phe Ala Arg Asp Ala Val Lys Lys Cys Phe Ala Val Cys Leu Ala
 145 150 155 160

<210> 11

<211> 1941

<212> DNA

<213> Homo sapiens

<400> 11

atggetgagg agggaggcgcc taagaagtcc cgggccgcgc gcggtggcgc gagctgggaa 60
 ctttgtgccg gggegtcttc ggcccggtg acggaggagg gcagcgggga cgccggtggc 120
 cgccgccgcc cgccagttga ccccgggcga ttggcgcgcc agctgctgct gctgctttgg 180
 ctgctggagg ctccgctgct gctgggggtc cgggccagc cggcgggcca ggggccaggc 240
 caggggcccg ggccggggca gcaaccgcc cggccgcctc agcagcaaca gagcgggcag 300
 cagtacaacg gcgagcgggg catctccgtc ccggaccacg gctattgcca gcccatctcc 360
 atcccgtgt gcacggacat cgcgtacaac cagaccatca tgcccaacct gctggggccac 420
 acgaaccagg aggacgcggg cctggaggtg caccagttct accctctagt gaaagtgcag 480
 tgttccgctg agctcaagtt cttcctgtgc tccatgtaac cgcccggtg caccgtgcta 540

16/233

gagcaggcgc tgcgcgcctg ccgctccctg tgcgagcgcg cgcgccaggg ctgcgaggcg 600
 etcatgaaca agttcggctt ccagtggcca gacacgetca agtgtgagaa gttcccgggtg 660
 cacggcgccg gcgagctgtg cgtggggccag aacacgtccg acaagggcac cccgacgccc 720
 tcgctgcttc cagagttctg gaccagcaac cctcagcacg gcggcggagg gcaccgtggc 780
 ggcttcccgg ggggcgcgg cgctcggag cgaggcaagt tctcctgccc gcgcgccttc 840
 aaggtgccct cctacctcaa ctaccacttc ctgggggaga aggactgcgg cgcaccttgt 900
 gagccgacca aggtgtatgg gctcatgtac ttccggcccg aggagctgcg cttctcgcgc 960
 acctggattg gcatttggtc agtgcgtgtc tgcgcctcca cgctcttcac ggtgcttacg 1020
 tacttggtgg acatgcggcg cttcagctac ccggagcggc ccatcatctt cttgtccggc 1080
 tgttacacgg ccgtggccgt ggcctacatc gccggcttcc tctggaaga ccgagtgggtg 1140
 tgtaatgaca agttcgccga ggacggggca cgcactgtgg cgcagggcac caagaaggag 1200
 ggctgcacca tctcttcat gatgctctac ttcttcagca tggccagctc catctgggtg 1260
 gtgatcctgt cgtcacctg gtctcctggcg gctggcatga agtggggcca cgaggccatc 1320
 gaagccaact cacagtattt tcacctggcc gcctgggctg tgcggccat caagaccatc 1380
 accatcctgg cgtggggcca ggtggacggc gatgtgctga gcggagtgtg cttcgtgggg 1440
 cttacaacg tggacgcgt gcgtggettc gtgctggcgc cctcttcgt gtacctgttt 1500
 atcggcacgt cttttctgt ggccggcttt gtgtcgtct tccgcatccg caccatcatg 1560
 aagcacgatg gcaccaagac cgagaagctg gagaagctca tggcgcat tggcgtcttc 1620
 agcgtgctgt aactgtgcc agccaccatc gtcacgcct gctacttcta cgagcaggcc 1680
 ttccgggacc agtgggaacg cagctgggtg gccagagct gcaagageta cgtatcccc 1740
 tgcctcacc tccaggcggg cggaggcgcc ccgcgcacc cggccatgag cccggacttc 1800
 acggtcttca tgattaagta ccttatgacg ctgacgtgg gcacacgtc gggcttctgg 1860
 atctggctcg gcaagacct caactcctgg aggaagttct acacgaggct caccaacagc 1920
 aaacaagggg agactacagt c 1941

<210> 12

<211> 1050

<212> DNA

<213> Homo sapiens

<400> 12

atgcacctg cagccttccc gcttctgtg gttgtggccg ctgtgctgtg gggagcggcc 60
 ccgacccggg ggctcattcg agcgacctcg gaccacaatg ccagcatgga ctttgacagc 120
 cttccagctc tgtttggggc taccttgagc caggagggcc tccaggggtt ccttgtggag 180
 gctcaccag acaatgcctg cagccccatt gccccaccac cccagcccc ggtcaatggg 240
 tcagtcttta ttgcgtgct tcgaagatc gactgcaact ttgacctca ggtcctaaat 300

17/233

```

gcccagaagg ctggatatgg tgcgctgta gtacacaatg tgaattccaa tgaacttctg 360
aacatggtgt ggaatagtga ggaaatccag cagcagatct ggatcccgtc tgtattttatt 420
ggggagagaa gctccgagta cctgcgtgcc ctctttgtct acgagaaggg ggctcgggtg 480
cttotggttc cagacaatac cttccccttg ggetattacc tcatcccctt cacagggatt 540
gtgggactgc tggttttggc catgggagca gtaatgatag ctggttgat ccagcaccgg 600
aaacggctcc agcggaatcg acttaccaaa gagcaactga aacagattcc tacacatgac 660
tatcagaagg gagaccagta tgatgtctgt gccatttgcc tggatgaata tgaggatggg 720
gacaagctgc gggtaactcc ctgtgctcat gcctaccaca gccgtgcgt ggacccttg 780
ctcactcaga cccggaagac ctgccccatt tgcaagcagc ctgttcacgc gggtcctggg 840
gacgaagacc aagaggaaga aactcaaggg caagaggagg gtgatgaagg ggagccaagg 900
gaccacctg cctcagaaag gacccactt ttgggtteta gcccactct tcccacctc 960
tttggttct tagccccagc tccccttgtt ttctctgggc cttcaacaga tccccactg 1020
tcccctcct cttcccctgt tctctgggc 1050

```

<210> 13

<211> 618

<212> DNA

<213> Homo sapiens

<400> 13

```

atggggctgg gtcagcccca ggctggttg ctgggtctgc ccacagctgt ggtctatggc 60
tccctggctc tottcaccac catcctgcac aatgtcttcc tgcttacta tgtggacacc 120
tttgtctcag tgtacaagat caacaaaatg gccttctggg tcggagagac agtgtttctc 180
ctctggaaca gcctcaatga cccctcttcc ggttggtctc gtgaccggca gttcctcagc 240
tcccagcccc ggggaagaga totaccctgg cttggcttgg ttggccctc tggactgtgg 300
actgcaaca cctctgctg cttctggaag attccttgc ccatccctg cttgagcccc 360
tcatcaccac caaccttgag aagtgggcat cccataccct ttggccatca gcccaacagg 420
ctaataaggg ggtggaaatt ggggcagagg aggagagtgt acccactggg caggcgccgg 480
gctctcctca agggctgtgg tctggcccgg ggtgcaggcc ctgggctggc atgggcccgt 540
gctggcctg tegtctctgg cgttctgggt gccctgggccc ccagctggcc tgcagttctt 600
gctgtgcctg tgcctcta 618

```

<210> 14

<211> 639

<212> DNA

<213> Homo sapiens

18/233

<400> 14

atgcactatt atagatactc taacgccaaag gtcagctgct ggtacaagta cctccttttc	60
agctacaaca tcatcttctg gttggtgga gttgtcttcc ttggagtcgg gctgtgggca	120
tggagcgaaa aggggtgtgt gtcggacctc accaaagtga cccggatgca tggaaatcgac	180
cctgtggtgc tggctctgat ggtgggcgtg gtgatgttca ccctgggggt cgccggctgc	240
gtgggggctc tgcgggagaa tatctgcttg ctcaacttta accagtgtgt tggcgcatat	300
ggccctgaag actgggacct caacgtctac ttcaattgca gcggtgccag ctacagccga	360
gagaagtgcg gggctccctt ctctgtgtgc gtgccagatc ctgcgcaaaa agttgtgaac	420
acacagtgtg gatatgatgt caggattcag ctgaagagca agtgggatga gtccatcttc	480
acgaaaggct gcatccaggc gctggaaagc tggctcccg cgaacattta cattgtggct	540
ggcgtcttca tcgccatctc gctgttgca atatttgga tcttctggc aaggacgctg	600
atctcagaca tcgaggcagt gaaggccgc catcacttc	639

<210> 15

<211> 1785

<212> DNA

<213> Homo sapiens

<400> 15

atgcgcgctg cccgcgcgc gccgtgtctc cagctgtgtc tcctgtggg gccgtggctg	60
gaggctgcgg gcgttgcgga gtgcgcgtg cccgcgtgg tccttgccat cctggccgcg	120
aatgccgaac actcgtgtcc cactacctg ggcgtcttg agcggctgga ctacccccg	180
gccaggatgg ccctctggtg tgccacggac cacaatgtgg acaacaccac agagatgctg	240
caggagtggc tggcggctgt gggcgatgac tatgtgtgtg tggcttgag gcctgagggc	300
gagcccaggt totaccaga tgaagagggt cccaagcact ggaccaaaga aaggcaccag	360
tttctgatgg agctgaagca ggaagccctc accttgcca ggaactggg ggcgcactat	420
atcctgtttg cagacacaga caacattctg accaacaatc agactctgcg gcttctcatg	480
gggcaggggc ttccagtgtt ggcccaatg ctggactccc agacctacta ctccaaactc	540
tgggtgtgga tcacccccca gggctactac cgcgcacag ccgagtactt cccaccaaag	600
aaccgccagc gccggggctg cttccgtgtc cccatggtcc actccacctt ccttgcatcc	660
ctgcgggctg aaggggcaga ccagcttgtt ttctaccgc cactcccaa ctacacttgg	720
cctttcgacg acatcatcgt ctgcctat gcctgccagg ctgctggggt ctccgtccac	780
gtgtgcaatg agcaccgtta tgggtacatg aatgtgccg tgaaatccca ccaggggctg	840
gaagacgaga gggctcaact catccacctg atcttagaag cactagtgga cgccccccgc	900
atgcaggcct cagctcatgt gactcgccc tctaagagg ccagcaagat agggtttgac	960
gaggcttttg tcatcagcct ggtcgcagg cctgaccgtc ggaacgcct gctcgcctcg	1020

19/233

ctctgggaga tggagatctc tgggaggggtg gtggacgctg tggatggctg gatgctcaac 1080
 agcagtgccca tcaggaacct cggcgtagac ctgctcccg gctaccagga cccttactcg 1140
 ggccgcactc tgaccaaggg cgaggtgggc tgccttctca gccattactc catctgggaa 1200
 gaggtggttg ccaggggcct ggcccgggtc ctggtgtttg aggatgacgt gcgctttgag 1260
 agcaacttca gggggcggtt ggagcggctg atggaggatg tggaggcaga gaaactgtct 1320
 tgggacctga tctacctcg acggaagcag gtgaaccctg agaaggagac ggccgtggag 1380
 gggctgccgg gcctggtggt ggctgggtac tcctactgga cgctggccta tgccctgcgt 1440
 ctggcgggtg cccgcaagct gctggcctca cagcctctgc gccgcattgct gcccgaggac 1500
 gagttcctgc ccattcatgtt cgaccagcac cccaacgagc agtacaaggc acaacttctgg 1560
 ccacgggacc tgggtggcctt ctccgcccag cccctgctcg ctgcccctac ccactatgcc 1620
 ggggacgccg agtggctcag tgacacggag acatcctctc catgggatga tgacagcggc 1680
 cgcctcatca gctggagcgg ctcccaaaaag accctgcgca gccccgcct ggacctgact 1740
 ggcagcagcg ggcacagcct ccaaccccag ccccgagatg agctc 1785

<210> 16

<211> 792

<212> DNA

<213> Homo sapiens

<400> 16

atggtggcct cagcgaagat gggccgggca gggaccatgg cgggtggcagc agagcttcga 60
 gagctgtgcc caggagtga caaccagccc tacctctgtg agagtggcga ctgctgcggg 120
 gagactggct gctgcacctc ctactatgag ctctggtggt tctggctgct ctggactgtc 180
 ctcatcctct ttagctgctg ttgcgccttc cgccaccgac gagctaaact caggctgcaa 240
 caacagcagc ggcagcgtga aatcaacttg ttggcctatc atggggcatg ccattggggt 300
 ggtcctttcc ctaccggttc actgcttgac cttegttcc tcagcacctt caagccccca 360
 gcctacgagg atgtggttca ccgcccaggc acaccacccc ccccttatac tgtggcccca 420
 ggccgcccct tgactgcttc cagtgaacaa acctgctgtt cctcctcctc cagctgccct 480
 gcccactttg aaggaacaaa tgtggaaggt gtttcctccc accagagtgc cccccccat 540
 caggaggggt agccccgggc aggggtgacc cctgcctcca cccccctc ctgcgctat 600
 cgccgtttaa ctggcgactc cgggtattgag ctctgccctt gtctgcctc cgggtgaggt 660
 gagccagtca aggaggtgag ggttagtgcc acctgcccag atctggagga ctactccccg 720
 tgtgcactac cccagagtc tgtaccgcag atctttccca tggggctgtc ttccagtga 780
 ggggacatcc ca 792

<210> 17

20/233

<211> 1029

<212> DNA

<213> Homo sapiens

<400> 17

atgcagcccc	cgcccccg	cccgtggg	gactgcctgc	gggactggga	ggatctacag	60
caggacttcc	agaacatcca	ggagacccat	cggtctctacc	gcctgaagct	ggaggagctg	120
accaaacttc	agaacaattg	caccagctcc	atcacgcggc	agaagaagcg	gctccaggag	180
ctggccctcg	ccctgaagaa	atgcaaacc	tccctcccag	cagaggccga	gggggcccga	240
caggagctgg	agaaccagat	gaaagagcgc	caaggcctct	tctttgacat	ggaggcctat	300
ttgcctaaga	agaatggatt	gtacctgagc	ctggtttctg	ggaacgtcaa	cgtcacgctc	360
ctgagcaagc	aggctaagtt	tgcctacaag	gacgagtatg	agaagttcaa	gctctacctc	420
accatcatcc	tcctctcat	ctccttcaact	tgcctcttcc	tgtctcaactc	cagggtgaca	480
gatgctgct	tcaacttcct	gctgggtctg	tactactgca	ccctgaccat	ccgggagagc	540
atcctcatca	acaacggctc	ccggatcaaa	ggctgggtgg	tgttccatca	ctacgtgtcc	600
accttctgt	cgggagtcat	gctgacgtgg	ccgacggtc	tcattgtacca	gaaattccgg	660
aaccaattcc	tctccttttc	catgtaccag	agcttcgtgc	agtttctcca	gtactactac	720
cagagcggct	gcctctaccg	cctgcggggc	ctgggcgagc	ggcacaccat	ggacctcact	780
gtggagggct	tccagtctcg	gatgtggcgg	ggctcacct	tcctgctgcc	ttttcttttc	840
tttggaact	tctggcagct	ttttaacgcg	ctgacgttgt	tcaacctggc	ccaggaccct	900
cagtgaagg	agtggcaggt	gcttatgtgc	ggctttccct	tcctcctcct	tttctcggc	960
aatttcttca	ccacctgag	ggttgtgcac	cacaagtttc	acagtcagcg	gcacgggagc	1020
aagaaggat						1029

<210> 18

<211> 732

<212> DNA

<213> Homo sapiens

<400> 18

atggacatcc	tggtcccact	cctgcagctg	ctggtgctgc	ttcttaccct	gccctgcac	60
ctcatggctc	tgtgggctg	ctggcagccc	ctgtgcaaaa	gctacttccc	ctacctgatg	120
gccgtgctga	ctcccaagag	caaccgcaag	atggagagca	agaaacggga	gctcttcagc	180
cagataaagg	ggcttacagg	agcctccggg	aaagtggccc	tactggagct	gggtgcgga	240
accggagcca	actttcagtt	ctaccaccg	ggctgcaggg	tcacctgcct	agacccaaat	300
ccccactttg	agaagtccct	gacaaagagc	atggctgaga	acaggcacct	ccaatatgag	360
cggtttgtgg	tggctcctgg	agaggacatg	agacagctgg	ctgatggctc	catggatgtg	420

21/233

gtggtctgca ctctggtgct gtgctctgtg cagagcccaa ggaaggtcct gcaggaggtc 480
 cggagagtagc tgagaccggg aggtgtgctc tttttctggg agcatgtggc agaaccatat 540
 ggaagctggg ccttcatgtg gcagcaagtt ttcgagccca cctggaaaca cattggggat 600
 ggctgctgcc tcaccagaga gacctggaag gatcttgaga acgcccagtt ctccgaaatc 660
 caaatggaac gacagccccc tcccttgaag tggtacctg ttgggccccca catcatggga 720
 aaggctgtca aa 732

<210> 19

<211> 909

<212> DNA

<213> Homo sapiens

<400> 19

atgaagetga agctgaagaa cgtgtttctc gcctacttcc tgggtgctgat cgccggcctc 60
 ctctacgcgc tggtagagct cggccagcca tgtgactgcc ttctcccct gcgggcagca 120
 gccgagcagc tacggcagaa ggatctgagg atttcccagc tgcaagcggg actccgacgg 180
 ccacccccctg cccctgccca gccccctgaa cccgaggccc tgctactat ctatgttggt 240
 acccccacct atgccaggcc cctgtgggtg cagtaccctc aggatgtgac taccttcaat 300
 atagatgata agtacttgct tggggatgag ttgctgggtc accctgtatc agactctgga 360
 gcccatggtg tccaggtcta tctgcctggc caaggggagg tgtggtatga cattcaaagc 420
 taccagaagc atcatggtcc ccagaccctg tacctgcctg taactetaag cagtatccct 480
 gtgttcacgc gtggaggagc aatcgtgcct cgatggatgc gagtgcggcg gtcttcagaa 540
 tgtatgaagg atgaccccat cactctcttt gttgcaacta gccctcaggg tacagctcaa 600
 ggagagctct ttctggatga tgggcacacg ttcaactatc agactcgcca agagttcctg 660
 ctgcgtcgat tctcattctc tggcaacacc cttgtctcca gctcagcaga cctgaagga 720
 cactttgaga caccaatctg gattgagcgg gtggtgataa taggggctgg aaagccagca 780
 gctgtggtac tccagacaaa aggatctcca gaaagccgcc tgctcttcca gcatgacct 840
 gagacctctg tgttggtcct gcgcaagcct ggcataaatg tggcatctga ttggagtatt 900
 cacctgcga 909

<210> 20

<211> 480

<212> DNA

<213> Homo sapiens

<400> 20

atggacaagc tgaagaaggc gctgagcggg caggacacgg aggaccggag cggcctgtcc 60

22/233

gaggttggtg aggcattctc attaagetgg agtaccagga taaaaggctt cattgcgtgt 120
 tttgctatag gaattctctg ctcaactgtg ggtactgttc tgctgtgggt gccaggaag 180
 ggactacacc tcttcgcagt gttttatacc tttggtaata tcgcatcaat tgggagtacc 240
 atcttcctca tgggaccagt gaaacagctg aagcgaatgt ttgagcctac tcgtttgatt 300
 gcaactatca tgggtgctgt gtgttttgca cttacctgt gttctgcctt ttggtggcat 360
 aacaagggac ttgcacttat cttctgcatt ttgcagctct tggcattgac gtggtacagc 420
 ctttccttca taccatttgc aagggatgct gtgaagaagt gttttgcctg gtgtcttgca 480

<210> 21

<211> 4485

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (189)...(2132)

<400> 21

gaatcgcaag tttccgcggc ggccggcggt gcggtacgca gaacaggagc cgggggagcg 60
 ggccgaaagc ggcttgggct cgacggaggg caccgcgcga gaggtctccc tggccgcagg 120
 gggagccgcc gccggcctg cccctggcag cccagcgga gcggcgccaa gagaggagcc 180
 gagaaagt atg gct gag gag gag gcg cct aag aag tcc cgg gcc gcc ggc 230
 Met Ala Glu Glu Glu Ala Pro Lys Lys Ser Arg Ala Ala Gly
 1 5 10
 ggt ggc gcg agc tgg gaa ctt tgt gcc ggg gcg ctc tcg gcc cgg ctg 278
 Gly Gly Ala Ser Trp Glu Leu Cys Ala Gly Ala Leu Ser Ala Arg Leu
 15 20 25 30
 acg gag gag ggc agc ggg gac gcc ggt ggc cgc cgc cgc ccg cca gtt 326
 Thr Glu Glu Gly Ser Gly Asp Ala Gly Gly Arg Arg Arg Pro Pro Val
 35 40 45
 gac ccc cgg cga ttg gcg cgc cag ctg ctg ctg ctg ctt tgg ctg ctg 374
 Asp Pro Arg Arg Leu Ala Arg Gln Leu Leu Leu Leu Trp Leu Leu
 50 55 60
 gag gct ccg ctg ctg ctg ggg gtc cgg gcc cag gcg gcg ggc cag ggg 422
 Glu Ala Pro Leu Leu Leu Gly Val Arg Ala Gln Ala Ala Gly Gln Gly
 65 70 75
 cca ggc cag ggg ccc ggg ccg ggg cag caa ccg ccg ccg ccg cct cag 470

23/233

Pro Gly Gln Gly Pro Gly Pro Gly Gln Gln Pro Pro Pro Pro Gln	
80 85 90	
cag caa cag agc ggg cag cag tac aac ggc gag cgg ggc atc tcc gtc	518
Gln Gln Gln Ser Gly Gln Gln Tyr Asn Gly Glu Arg Gly Ile Ser Val	
95 100 105 110	
ccg gac cac ggc tat tgc cag ccc atc tcc atc ccg ctg tgc acg gac	566
Pro Asp His Gly Tyr Cys Gln Pro Ile Ser Ile Pro Leu Cys Thr Asp	
115 120 125	
atc gcg tac aac cag acc atc atg ccc aac ctg ctg ggc cac acg aac	614
Ile Ala Tyr Asn Gln Thr Ile Met Pro Asn Leu Leu Gly His Thr Asn	
130 135 140	
cag gag gac gcg ggc ctg gag gtg cac cag ttc tac cct cta gtg aaa	662
Gln Glu Asp Ala Gly Leu Glu Val His Gln Phe Tyr Pro Leu Val Lys	
145 150 155	
gtg cag tgt tcc gct gag ctc aag ttc ttc ctg tgc tcc atg tac gcg	710
Val Gln Cys Ser Ala Glu Leu Lys Phe Phe Leu Cys Ser Met Tyr Ala	
160 165 170	
ccc gtg tgc acc gtg cta gag cag gcg ctg ccg ccc tgc cgc tcc ctg	758
Pro Val Cys Thr Val Leu Glu Gln Ala Leu Pro Pro Cys Arg Ser Leu	
175 180 185 190	
tgc gag cgc gcg cgc cag ggc tgc gag gcg ctc atg aac aag ttc ggc	806
Cys Glu Arg Ala Arg Gln Gly Cys Glu Ala Leu Met Asn Lys Phe Gly	
195 200 205	
ttc cag tgg cca gac acg ctc aag tgt gag aag ttc ccg gtg cac ggc	854
Phe Gln Trp Pro Asp Thr Leu Lys Cys Glu Lys Phe Pro Val His Gly	
210 215 220	
gcc ggc gag ctg tgc gtg ggc cag aac acg tcc gac aag ggc acc ccg	902
Ala Gly Glu Leu Cys Val Gly Gln Asn Thr Ser Asp Lys Gly Thr Pro	
225 230 235	
acg ccc tcg ctg ctt cca gag ttc tgg acc agc aac cct cag cac ggc	950
Thr Pro Ser Leu Leu Pro Glu Phe Trp Thr Ser Asn Pro Gln His Gly	
240 245 250	
ggc gga ggg cac cgt ggc ggc ttc ccg ggg ggc gcc ggc gcg tcg gag	998
Gly Gly Gly His Arg Gly Gly Phe Pro Gly Gly Ala Gly Ala Ser Glu	
255 260 265 270	

24/233

cga ggc aag ttc tcc tgc ccg cgc gcc ctc aag gtg ccc tcc tac ctc	1046
Arg Gly Lys Phe Ser Cys Pro Arg Ala Leu Lys Val Pro Ser Tyr Leu	
275 280 285	
aac tac cac ttc ctg ggg gag aag gac tgc ggc gca cct tgt gag ccg	1094
Asn Tyr His Phe Leu Gly Glu Lys Asp Cys Gly Ala Pro Cys Glu Pro	
290 295 300	
acc aag gtg tat ggg ctc atg tac ttc ggg ccc gag gag ctg cgc ttc	1142
Thr Lys Val Tyr Gly Leu Met Tyr Phe Gly Pro Glu Glu Leu Arg Phe	
305 310 315	
tcg cgc acc tgg att ggc att tgg tca gtg ctg tgc tgc gcc tcc acg	1190
Ser Arg Thr Trp Ile Gly Ile Trp Ser Val Leu Cys Cys Ala Ser Thr	
320 325 330	
ctc ttc acg gtg ctt acg tac ctg gtg gac atg cgg cgc ttc agc tac	1238
Leu Phe Thr Val Leu Thr Tyr Leu Val Asp Met Arg Arg Phe Ser Tyr	
335 340 345 350	
ccg gag cgg ccc atc atc ttc ttg tcc ggc tgt tac acg gcc gtg gcc	1286
Pro Glu Arg Pro Ile Ile Phe Leu Ser Gly Cys Tyr Thr Ala Val Ala	
355 360 365	
gtg gcc tac atc gcc ggc ttc ctc ctg gaa gac cga gtg gtg tgt aat	1334
Val Ala Tyr Ile Ala Gly Phe Leu Leu Glu Asp Arg Val Val Cys Asn	
370 375 380	
gac aag ttc gcc gag gac ggg gca cgc act gtg gcg cag gcc acc aag	1382
Asp Lys Phe Ala Glu Asp Gly Ala Arg Thr Val Ala Gln Gly Thr Lys	
385 390 395	
aag gag ggc tgc acc atc ctc ttc atg atg ctc tac ttc ttc agc atg	1430
Lys Glu Gly Cys Thr Ile Leu Phe Met Met Leu Tyr Phe Phe Ser Met	
400 405 410	
gcc agc tcc atc tgg tgg gtg atc ctg tgc ctc acc tgg ttc ctg gcg	1478
Ala Ser Ser Ile Trp Trp Val Ile Leu Ser Leu Thr Trp Phe Leu Ala	
415 420 425 430	
gct ggc atg aag tgg ggc cac gag gcc atc gaa gcc aac tca cag tat	1526
Ala Gly Met Lys Trp Gly His Glu Ala Ile Glu Ala Asn Ser Gln Tyr	
435 440 445	
ttt cac ctg gcc gcc tgg gct gtg ccg gcc atc aag acc atc acc atc	1574
Phe His Leu Ala Ala Trp Ala Val Pro Ala Ile Lys Thr Ile Thr Ile	

25/233

450	455	460	
ctg gcg ctg ggc cag gtg gac ggc gat gtg ctg agc gga gtg tgc ttc			1622
Leu Ala Leu Gly Gln Val Asp Gly Asp Val Leu Ser Gly Val Cys Phe			
465	470	475	
gtg ggg ctt aac aac gtg gac gcg ctg cgt ggc ttc gtg ctg gcg ccc			1670
Val Gly Leu Asn Asn Val Asp Ala Leu Arg Gly Phe Val Leu Ala Pro			
480	485	490	
ctc ttc gtg tac ctg ttt atc ggc acg tcc ttt ctg ctg gcc ggc ttt			1718
Leu Phe Val Tyr Leu Phe Ile Gly Thr Ser Phe Leu Leu Ala Gly Phe			
495	500	505	510
gtg tcg ctc ttc cgc atc cgc acc atc atg aag cac gat ggc acc aag			1766
Val Ser Leu Phe Arg Ile Arg Thr Ile Met Lys His Asp Gly Thr Lys			
515	520	525	
acc gag aag ctg gag aag ctc atg gtg cgc att ggc gtc ttc agc gtg			1814
Thr Glu Lys Leu Glu Lys Leu Met Val Arg Ile Gly Val Phe Ser Val			
530	535	540	
ctg tac act gtg cca gcc acc atc gtc atc gcc tgc tac ttc tac gag			1862
Leu Tyr Thr Val Pro Ala Thr Ile Val Ile Ala Cys Tyr Phe Tyr Glu			
545	550	555	
cag gcc ttc cgg gac cag tgg gaa cgc agc tgg gtg gcc cag agc tgc			1910
Gln Ala Phe Arg Asp Gln Trp Glu Arg Ser Trp Val Ala Gln Ser Cys			
560	565	570	
aag agc tac gct atc ccc tgc cct cac ctc cag gcg ggc gga ggc gcc			1958
Lys Ser Tyr Ala Ile Pro Cys Pro His Leu Gln Ala Gly Gly Gly Ala			
575	580	585	590
ccg ccg cac ccg ccc atg agc ccg gac ttc acg gtc ttc atg att aag			2006
Pro Pro His Pro Pro Met Ser Pro Asp Phe Thr Val Phe Met Ile Lys			
595	600	605	
tac ctt atg acg ctg atc gtg ggc atc acg tcg ggc ttc tgg atc tgg			2054
Tyr Leu Met Thr Leu Ile Val Gly Ile Thr Ser Gly Phe Trp Ile Trp			
610	615	620	
tcc ggc aag acc ctc aac tcc tgg agg aag ttc tac acg agg ctc acc			2102
Ser Gly Lys Thr Leu Asn Ser Trp Arg Lys Phe Tyr Thr Arg Leu Thr			
625	630	635	
aac agc aaa caa ggg gag act aca gtc tgagacccgg ggctcagccc a			2150

26/233

Asn Ser Lys Gln Gly Glu Thr Thr Val

640

645

tgcccaggcc	tgggcccggg	cgcagcgate	ccccaaagcc	agcgcctggt	agttcgtgcc	2210
aatcctgaca	tctcgagggt	tcttcactag	acaactctct	ttcgcagget	cctttgaaca	2270
actcagctcc	tgcaaaagct	tccgtccctg	aggcaaaagg	acacgagggc	cgcactgcca	2330
gagggaggat	ggacagacct	cttgccctca	cactctggta	ccaggactgt	tcgcttttat	2390
gattgtaaat	agcctgtgta	agatttttgt	aagtatatatt	gtatttaaata	gacgaccgat	2450
cacgcgtttt	tctttttcaa	aagtttttaa	ttatttaggg	cggtttaacc	atttgaggct	2510
tttctctctt	gccctttctg	gagtattgca	aaggagctaa	aactggtgtg	caaccgcaca	2570
gcgctcctgg	tcgtcctcgc	gcgcctctcc	ctaccacggg	tgctcgggac	ggctggggcg	2630
cagctccggg	gcgagttcag	cactgcgggg	tgcgactagg	gctgcgctgc	cagggtcact	2690
tcccgctccc	tccttttgcc	ccctcccccct	ccttctgtcc	cctccctttc	tttctggtct	2750
tgaggtaggg	gctcttaagg	tacagaactc	cacaaacctt	ccaaatctgg	aggagggccc	2810
ccatacatta	caattcctcc	cttgctcggc	ggtggattgc	gaaggcccgt	cccttcgact	2870
tctgaagct	ggatttttaa	ctgtccagaa	ctttcctcca	acttcattgg	ggcccacggg	2930
tgtgggcgct	ggcagctcca	gcctccctcc	acggtcacct	tcaacgcccc	gacactccct	2990
tctccacact	tagttggtta	caggggtgagt	gagataacca	atgccaaact	ttttgaagtc	3050
taatttttga	ggggtgagct	catttcattc	tctagtgtct	aaaacctggt	atgggtttgg	3110
ccagcgtcat	ggaaagatgt	ggttactgag	atttgggag	aagcatgaag	ctttgtgtgg	3170
gttggaagag	actgaagata	tgggttataa	aatgttaatt	ctaattgcat	acggatgcct	3230
ggcaaccttg	cctttgagaa	tgagacagcc	tgcgcttaga	ttttaccggt	ctgtaaaatg	3290
gaaatgttga	ggtcacctgg	aaagctttgt	taaggagtgt	atgtttgctt	tccttaacaa	3350
gacagcaaaa	cgtaaacaga	aattgaaaac	ttgaaggata	tttcagtgtc	atggacttcc	3410
tcaaaatgaa	gtgctatttt	cttattttta	atcaaataac	tagacatata	tcagaaactt	3470
taaaatgtaa	aagttgtaca	ctttcaacat	tttattacga	ttattattca	gcagcacatt	3530
ctgagggggg	aacaattcac	accaccaata	ataacctggt	aagatttcag	gaggtaaaga	3590
aggtggaata	attgacgggg	agatagcgcc	tgaaataaac	aaaatatggg	catgcatgct	3650
aaagggaaaa	tgtgtgcagg	tctactgcat	taaatcctgt	gtgtcctctt	tttggtttta	3710
cagaaatgtg	tcaaatgtaa	atctttcaaa	gccatttaaa	aatattcact	ttagttctct	3770
gtgaagaaga	ggagaaaagc	aatcctcctg	attgtattgt	tttaaaacttt	aagaatttat	3830
caaaatgccg	gtacttagga	cctaaattta	tctatgtctg	tcatacgcta	aaatgatatt	3890
ggtctttgaa	tttggtatac	atttattctg	ttcactatca	caaaatcctc	tatattttata	3950
gaggaataga	agttttatata	tatataatac	catattttta	atttcacaaa	taaaaaattc	4010
aaagttttgt	acaaaattat	atggattttg	tgcttgaaaa	taatagagct	tgagctgtct	4070
gaactatttt	acatttttatg	gtgtctcata	gccaatcccc	cagtgtaaaa	attcaggaat	4130

27/233

tcaatgaaaa aagtctaccc ttaaaccctc agatcagtct ttccaaagaa ttactctgtt 4190
 tgcattgttg tgattgacat ttgtgaagtc ccaagaaaag atctgttttc atgacagtag 4250
 aaaatagaag ttgtgcaaatt atttctttac tcaaagagga ttaaaagaga actctaattt 4310
 taatattaaa gctttctttt ctttcaggga ataaatttac atgacttttt atattatgga 4370
 gggtttattt taaatcatca cttttctcat attttttaga ggtattgtct tatctcttcc 4430
 ataatcttgg atattacaaa accctaaata ggcaatcaat aaatggtaa ctggc 4485

<210> 22

<211> 1509

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (253)...(1305)

<400> 22

ttttccgcgt tttatccccg taccagaaaa ggatacattt agtgccctccc acccagctcc 60
 actaaacggg ttggatatct cattctttga gttggtgttc cttccccggc gcccccatgt 120
 agctgggaag tgggacctgg ggggtggttg acccctggga tcttaaagga ggggcaggga 180
 ggggcagaaa ctccgcttct gctccttget accaggacgc gcggcctcct cagcctcttt 240
 cctcccgctg cc atg cac cct gca gcc ttc ccg ctt cct gtg gtt gtg gcc 291
 Met His Pro Ala Ala Phe Pro Leu Pro Val Val Val Ala
 1 5 10
 gct gtg ctg tgg gga gcg gcc ccg acc cgg ggg ctc att cga gcg acc 339
 Ala Val Leu Trp Gly Ala Ala Pro Thr Arg Gly Leu Ile Arg Ala Thr
 15 20 25
 tcg gac cac aat gcc agc atg gac ttt gca gac ctt cca gct ctg ttt 387
 Ser Asp His Asn Ala Ser Met Asp Phe Ala Asp Leu Pro Ala Leu Phe
 30 35 40 45
 ggg gct acc ttg agc cag gag ggc ctc cag ggg ttc ctt gtg gag gct 435
 Gly Ala Thr Leu Ser Gln Glu Gly Leu Gln Gly Phe Leu Val Glu Ala
 50 55 60
 cac cca gac aat gcc tgc agc ccc att gcc cca cca ccc cca gcc ccg 483
 His Pro Asp Asn Ala Cys Ser Pro Ile Ala Pro Pro Pro Pro Ala Pro
 65 70 75
 gtc aat ggg tca gtc ttt att gcg ctg ctt cga aga ttc gac tgc aac 531

28/233

Val Asn Gly Ser Val Phe Ile Ala Leu Leu Arg Arg Phe Asp Cys Asn	
80 85 90	
ttt gac ctc aag gtc cta aat gcc cag aag gct gga tat ggt gcc gct	579
Phe Asp Leu Lys Val Leu Asn Ala Gln Lys Ala Gly Tyr Gly Ala Ala	
95 100 105	
gta gta cac aat gtg aat tcc aat gaa ctt ctg aac atg gtg tgg aat	627
Val Val His Asn Val Asn Ser Asn Glu Leu Leu Asn Met Val Trp Asn	
110 115 120 125	
agt gag gaa atc cag cag cag atc tgg atc ccg tct gta ttt att ggg	675
Ser Glu Glu Ile Gln Gln Gln Ile Trp Ile Pro Ser Val Phe Ile Gly	
130 135 140	
gag aga agc tcc gag tac ctg cgt gcc ctc ttt gtc tac gag aag ggg	723
Glu Arg Ser Ser Glu Tyr Leu Arg Ala Leu Phe Val Tyr Glu Lys Gly	
145 150 155	
gct cgg gtg ctt ctg gtt cca gac aat acc ttc ccc ttg ggc tat tac	771
Ala Arg Val Leu Leu Val Pro Asp Asn Thr Phe Pro Leu Gly Tyr Tyr	
160 165 170	
ctc atc cct ttc aca ggg att gtg gga ctg ctg gtt ttg gcc atg gga	819
Leu Ile Pro Phe Thr Gly Ile Val Gly Leu Leu Val Leu Ala Met Gly	
175 180 185	
gca gta atg ata gct cgt tgt atc cag cac cgg aaa cgg ctc cag cgg	867
Ala Val Met Ile Ala Arg Cys Ile Gln His Arg Lys Arg Leu Gln Arg	
190 195 200 205	
aat cga ctt acc aaa gag caa ctg aaa cag att cct aca cat gac tat	915
Asn Arg Leu Thr Lys Glu Gln Leu Lys Gln Ile Pro Thr His Asp Tyr	
210 215 220	
cag aag gga gac cag tat gat gtc tgt gcc att tgc ctg gat gaa tat	963
Gln Lys Gly Asp Gln Tyr Asp Val Cys Ala Ile Cys Leu Asp Glu Tyr	
225 230 235	
gag gat ggg gac aag ctg cgg gta ctc ccc tgt gct cat gcc tac cac	1011
Glu Asp Gly Asp Lys Leu Arg Val Leu Pro Cys Ala His Ala Tyr His	
240 245 250	
agc cgc tgc gtg gac ccc tgg ctc act cag acc cgg aag acc tgc ccc	1059
Ser Arg Cys Val Asp Pro Trp Leu Thr Gln Thr Arg Lys Thr Cys Pro	
255 260 265	

29/233

```

att tgc aag cag cct gtt cat cgg ggt cct ggg gac gaa gac caa gag      1107
Ile Cys Lys Gln Pro Val His Arg Gly Pro Gly Asp Glu Asp Gln Glu
270                275                280                285
gaa gaa act caa ggg caa gag gag ggt gat gaa ggg gag cca agg gac      1155
Glu Glu Thr Gln Gly Gln Glu Glu Gly Asp Glu Gly Glu Pro Arg Asp
                290                295                300
cac cct gcc tca gaa agg acc cca ctt ttg ggt tct agc ccc act ctt      1203
His Pro Ala Ser Glu Arg Thr Pro Leu Leu Gly Ser Ser Pro Thr Leu
                305                310                315
ccc acc tcc ttt ggt tcc tta gcc cca gct ccc ctt gtt ttt cct ggg      1251
Pro Thr Ser Phe Gly Ser Leu Ala Pro Ala Pro Leu Val Phe Pro Gly
                320                325                330
cct tca aca gat ccc cca ctg tcc cct ccc tct tcc cct gtt atc ctg      1299
Pro Ser Thr Asp Pro Pro Leu Ser Pro Pro Ser Ser Pro Val Ile Leu
                335                340                345
gtc taataacccc ccacacatac acctctggtg acctatttgc acagaccg      1350
Val
350
tcgtcttccc tccagtcttc tgagggatag gggacattcc atcccaagct tctcccttac      1410
ccacacctat ccttttgagg ggctttgggg tggggctggg gcaagcagag ggactgggtc      1470
ttcacttctt gggctaataa aattgtttct ttgtggact      1509

```

<210> 23

<211> 3059

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (230)...(850)

<400> 23

```

cctggctccc gccagccgtg ggattagget tcgccggcta cgattgcggc ccccatcttc      60
tgacttttcc tcgtgtgacc catcttttca aattccetta cctgaggaag gagcccgatt      120
acaaggatat ttacctgtc ctacctgat ctaggacga ggatgggaag accgcctgtg      180
gccatgagcc ctccccggtg ctccctgggc taaggctggg gctgcagcc atg ggg ctg      238
Met Gly Leu

```

30/233

1

ggt cag ccc cag gcc tgg ttg ctg ggt ctg ccc aca gct gtg gtc tat	286
Gly Gln Pro Gln Ala Trp Leu Leu Gly Leu Pro Thr Ala Val Val Tyr	
5 10 15	
ggc tcc ctg gct ctc ttc acc acc atc ctg cac aat gtc ttc ctg ctc	334
Gly Ser Leu Ala Leu Phe Thr Thr Ile Leu His Asn Val Phe Leu Leu	
20 25 30 35	
tac tat gtg gac acc ttt gtc tca gtg tac aag atc aac aaa atg gcc	382
Tyr Tyr Val Asp Thr Phe Val Ser Val Tyr Lys Ile Asn Lys Met Ala	
40 45 50	
ttc tgg gtc gga gag aca gtg ttt ctc ctc tgg aac agc ctc aat gac	430
Phe Trp Val Gly Glu Thr Val Phe Leu Leu Trp Asn Ser Leu Asn Asp	
55 60 65	
ccc ctc ttc ggt tgg ctc agt gac egg cag ttc ctc agc tcc cag ccc	478
Pro Leu Phe Gly Trp Leu Ser Asp Arg Gln Phe Leu Ser Ser Gln Pro	
70 75 80	
egg gga aga gat cta ccc tgg ctt ggc ttg gtt ggc ccc tct gga ctg	526
Arg Gly Arg Asp Leu Pro Trp Leu Gly Leu Val Gly Pro Ser Gly Leu	
85 90 95	
tgg act gca aac acc ctc tgc tgc ttc tgg aag att cct ttg ccc cat	574
Trp Thr Ala Asn Thr Leu Cys Cys Phe Trp Lys Ile Pro Leu Pro His	
100 105 110 115	
ccc tgc ttg agc ccg tca tca ccc cca acc ttg aga agt ggg cat ccc	622
Pro Cys Leu Ser Pro Ser Ser Pro Pro Thr Leu Arg Ser Gly His Pro	
120 125 130	
ata ccc ttt ggc cat cag ccc aac agg cta ata agg ggg tgg aaa ttg	670
Ile Pro Phe Gly His Gln Pro Asn Arg Leu Ile Arg Gly Trp Lys Leu	
135 140 145	
ggg cag agg agg aga gtg tac cca ctg gtc agg cgc cgg gct ctc ctc	718
Gly Gln Arg Arg Arg Val Tyr Pro Leu Val Arg Arg Arg Ala Leu Leu	
150 155 160	
aag ggc tgt ggt gct ggc ccg ggt gca ggc cct ggg ctg gca tgg gcc	766
Lys Gly Cys Gly Ala Gly Pro Gly Ala Gly Pro Gly Leu Ala Trp Ala	
165 170 175	
gct gct ggc gct gtc gtt cct ggc gtt ctg ggt gcc ctg ggc ccc agc	814

31/233

Ala Ala Gly Ala Val Val Pro Gly Val Leu Gly Ala Leu Gly Pro Ser

180

185

190

195

tgg cct gca gtt ctt gct gtg cct gtg cct cta tgatggettc ctg

860

Trp Pro Ala Val Leu Ala Val Pro Val Pro Leu

200

205

acgctcgtgg acctgcacca ccatgccttg ctggccgacc tggccctctc agcccacgac 920

cgcacccacc tcaacttcta ctgctccctc ttcagcgagg cggctccct ctctgtcttt 980

gcatoctatg ccttttgga caaggaggat ttctcctcct tccgcgcttt ctgctgaca 1040

ctggtgtca gctctgggct gggctttctg ggggccacac agctgtgag gggcggggt 1100

gaggcggccc gaaaggacc aggtgtctca ggcctggttg tggatagcgg cctgtgtgga 1160

gaggagctgc ttgtaggcag tgaggaggcg gacagcatca cctggggccg gtatctccgg 1220

cagctggcac gccatcgga cttcctgttg ttctgtagca tggacctggt gcaggtcttc 1280

cactgccact tcaacagcaa cttcttcct ctcttcctgg agcatctgtt gtccgacct 1340

atctcccttt ccacgggctc catcctgttg ggcctctcct atgtcgtcc ccatctaac 1400

aacctctact tctgtccct gtgcgggcgc tggggcgctc acgcggtggt gcgggggctc 1460

ttctgtctca agctgggact tagcctgtc atgttggttg cgggcccgga ccacctcagc 1520

ctgtgtgcc tcttcattgc cagcaaccgc gtcttcactg agggcacctg taagctgtg 1580

accttggtgg tcactgacct ggtagacgag gacctggtgc tgaaccaccg caagcaggca 1640

gcctcggcac tctcttttg catggttgcc ttggtgacca agccaggcca gaccttgcc 1700

ccgtgtgtgg gcacctggt gctctgtttc tacacaggtc atgacctctt ccagcagtc 1760

ctcataacc ctgtggggag tgcccatccc tggccagagc cccagctcc agccctgca 1820

caggccccga cgctccgcca gggctgcttc tacctgtgtg tctgtgtgcc catcacctgt 1880

gctctgtgc agctcttcac ctggtcccag ttcacgtgc atgggagacg cctgcacatg 1940

gtcaaggccc agcgcagaa cctgtcacag gcccacccc tggatgttaa gatggtgtga 2000

gagctgtggc aaggtcaccc cactgaggat gctgtggca gcctggggaa ggagccagtt 2060

ttttttggtt ttttttttaa ggatttcata gttttttttt ttttttttg gagatgttg 2120

ccaaaaaat ggatctgttg cagtgttgca atctgggctc actgaaacca ccaccaggt 2180

tcaagcaatt atcctgcctc agcttcccga gtaggtggga ttataggagc gtgccaccat 2240

gcccggctac tttttgtatt tttagtagag acagggtttc atcatgttg ccaggetagt 2300

ctcaaacccc tgacctagg tgatcagccc gcctcggcct cccagagtgc tgggattaca 2360

ggcgtgagcc actgtggcca acctaat ttt tgtattattt agtagagaca gggtttcacc 2420

acattggcca ggetggtctc gaactcctga cctcaagtga tctgcctgcc ttggtctccc 2480

aaagtgtgg gaatacaggc atgagccacc gcactcggcc aggagctagt tttaccagca 2540

tcctgtcca ctgccttct ctagtgcagc ctggaagaca tggcagcggg tagctcctgg 2600

ggctgagcca gaagcatcac tgcaagtga gctctgtctt acctgtctgg ctcagcttgg 2660

32/233

gcaagggctg ggccatatgt gctcagggac gtgcttctct tgtaaggcag gaggatagaa 2720
 gaggaccaag aagggagggg gctgccctgt ggtgcacaca ggcccgccat ggggcgtggg 2780
 agcccatccc gctgcctgac tggagctggc cgctgtggtg gactcaggaa ccacttttaa 2840
 tactgcaact gctccctttt gccagtcag ggaaagctga ctgtaagtcc cacctcccac 2900
 tccgtccacc cttctagtgg tttctctgag aggtttctct gcttcagctg tgcttgaagt 2960
 ggcattgctc ctctgctgca gggtccccc acccccacac ggccctctaaa gatgtttatt 3020
 tccttataga ctgattaaag tcagccattc tttttctc 3059

<210> 24

<211> 2367

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (69)...(710)

<400> 24

aacttcctcg gccgagccgg gcgcgcgcgc cgctgccgcc gccgcgcgcg gattctgctt 60
 ctcagaag atg cac tat tat aga tac tct aac gcc aag gtc agc tgc tgg 110
 Met His Tyr Tyr Arg Tyr Ser Asn Ala Lys Val Ser Cys Trp
 1 5 10
 tac aag tac ctc ctt ttc agc tac aac atc atc ttc tgg ttg gct gga 158
 Tyr Lys Tyr Leu Leu Phe Ser Tyr Asn Ile Ile Phe Trp Leu Ala Gly
 15 20 25 30
 gtt gtc ttc ctt gga gtc ggg ctg tgg gca tgg agc gaa aag ggt gtg 206
 Val Val Phe Leu Gly Val Gly Leu Trp Ala Trp Ser Glu Lys Gly Val
 35 40 45
 ctg tcc gac ctc acc aaa gtg acc cgg atg cat gga atc gac cct gtg 254
 Leu Ser Asp Leu Thr Lys Val Thr Arg Met His Gly Ile Asp Pro Val
 50 55 60
 gtg ctg gtc ctg atg gtg ggc gtg gtg atg ttc acc ctg ggg ttc gcc 302
 Val Leu Val Leu Met Val Gly Val Val Met Phe Thr Leu Gly Phe Ala
 65 70 75
 ggc tgc gtg ggg gct ctg cgg gag aat atc tgc ttg ctc aac ttt aac 350
 Gly Cys Val Gly Ala Leu Arg Glu Asn Ile Cys Leu Leu Asn Phe Asn
 80 85 90

33/233

cag tgc tgt ggc gca tat ggc cct gaa gac tgg gac ctc aac gtc tac 398
 Gln Cys Cys Gly Ala Tyr Gly Pro Glu Asp Trp Asp Leu Asn Val Tyr
 95 100 105 110
 ttc aat tgc agc ggt gcc agc tac agc cga gag aag tgc ggg gtc ccc 446
 Phe Asn Cys Ser Gly Ala Ser Tyr Ser Arg Glu Lys Cys Gly Val Pro
 115 120 125
 ttc tcc tgc tgc gtg cca gat cct gcg caa aaa gtt gtg aac aca cag 494
 Phe Ser Cys Cys Val Pro Asp Pro Ala Gln Lys Val Val Asn Thr Gln
 130 135 140
 tgt gga tat gat gtc agg att cag ctg aag agc aag tgg gat gag tcc 542
 Cys Gly Tyr Asp Val Arg Ile Gln Leu Lys Ser Lys Trp Asp Glu Ser
 145 150 155
 atc ttc acg aaa ggc tgc atc cag gcg ctg gaa agc tgg ctc ccg cgg 590
 Ile Phe Thr Lys Gly Cys Ile Gln Ala Leu Glu Ser Trp Leu Pro Arg
 160 165 170
 aac att tac att gtg gct ggc gtc ttc atc gcc atc tcg ctg ttg cag 638
 Asn Ile Tyr Ile Val Ala Gly Val Phe Ile Ala Ile Ser Leu Leu Gln
 175 180 185 190
 ata ttt ggc atc ttc ctg gca agg acg ctg atc tca gac atc gag gca 686
 Ile Phe Gly Ile Phe Leu Ala Arg Thr Leu Ile Ser Asp Ile Glu Ala
 195 200 205
 gtg aag gcc ggc cat cac ttc tgaggagcag agttgaggga gccgagctga gcc 740
 Val Lys Ala Gly His His Phe
 210
 acgctgggag gccagagcct ttctctgccca tcagccctac gtccagaggg agaggagccg 800
 acacccccag agccagtgcc ccatcttaag catcagcgtg acgtgacctc tctgtttctg 860
 cttgctggtg ctgaagacca aggggtcccc ttgttacctg cccaaacttg tgactgcate 920
 cctctggagt ctacccagag acagagaatg tgtctttatg tgggagtggg gactctgaaa 980
 gacagagagg gctcctgtgg ctgccaggag ggcttgactc agacccccctg cagctcaagc 1040
 atgtctgcag gacaccctgg tcccctctcc actggcatcc agacatctgc tttgggtcat 1100
 ccacatctgt ggggtgggccc tgggtagagg gaccacagg cgtggacagg gcatctctct 1160
 ccatcaagca aagcagcatg ggggcctgcc cgtaacggga ggcggacgtg gccccgctgg 1220
 gctctgagt gccagcgcag tctgctggga catgcacata tcaggggttg tttgcaggat 1280
 cctcagccat gttcaagtga agtaagcctg agccagtgcg tggactggtg ccacgggagt 1340
 gccttgcca ctgtccccc gtgtccacca gctattctcc tggcgccgga actgcctctg 1400

34/233

```

gtcttgatag cattaagccc tgatggcgcc ggtggcgccg tgggcatggg tcttcaactga 1460
gagccggtct tccttttctt aaagtgtgta aatagtttat ttataggggt aagaatgttc 1520
tcacaccatt tcacttcttc ttctctctct ccagcattct cctctgagca gccttagata 1580
gtgtccatgg ctggagccga ccctttgagt ccccttgagt gtcttaagaa ccagcccaca 1640
acagcctctc tttctctctc acatactgca gcctccctcc atgcatccca catacaagca 1700
ctccccact cccagcgtg gcctcactgt cttctggtct tggtgctact gaaattgtca 1760
cccagaatth gaatcctgac cctccccact gcaagcccag ggagcccag cccaagatgg 1820
ccagcctgaa actgttgccc agggctctc ttgtggccat gtaccagggt ctggtggcc 1880
tgccatttgc ctctccccg agacagccgt tctctgcaa ccacccccg tgccatagcca 1940
caaccccagg ctgcagctgc tcagaagctc caggcatttt gttctggtg accgccccta 2000
atgggatata ggtgatcact ggtccacct tcctgtcagg gcttttctgg ggtgctctt 2060
ggaaatgaag tcttaagtac tgaataactc ccctggggat agctggggca tttgtctagc 2120
tggtgactct tctaactct tgccatagct cagaccactt ctcatcgctc agggatggac 2180
tgcaacctta atttacttgc cggagtgtac attctagtgt ggtgtatact ggtggctgtt 2240
gatgatgatt tttttttttt ttttttacac aattctctgt agactaggag aagaatgctt 2300
gtgtttttcg gaagtgtgat gcttctcttt gactgccaaa ctcttttatg gaatatct 2360
ttatatt 2367

```

<210> 25

<211> 2355

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (20)...(1807)

<400> 25

```

agccgcccaa gcgcccgc atg cgc gct gcc cgc gcc gcg ccg ctg ctc cag 52
Met Arg Ala Ala Arg Ala Ala Pro Leu Leu Gln
1 5 10
ctg ctg ctc ctg ctg ggg ccg tgg ctg gag gct gcg ggc gtt gcg gag 100
Leu Leu Leu Leu Leu Gly Pro Trp Leu Glu Ala Ala Gly Val Ala Glu
15 20 25
tcg ccg ctg ccc gcc gtg gtc ctt gcc atc ctg gcc cgc aat gcc gaa 148
Ser Pro Leu Pro Ala Val Val Leu Ala Ile Leu Ala Arg Asn Ala Glu
30 35 40

```

35/233

cac tgc ctg ccc cac tac ctg ggc gct ctg gag cgg ctg gac tac ccc	196
His Ser Leu Pro His Tyr Leu Gly Ala Leu Glu Arg Leu Asp Tyr Pro	
45 50 55	
cgg gcc agg atg gcc ctc tgg tgt gcc acg gac cac aat gtg gac aac	244
Arg Ala Arg Met Ala Leu Trp Cys Ala Thr Asp His Asn Val Asp Asn	
60 65 70 75	
acc aca gag atg ctg cag gag tgg ctg gcg gct gtg ggc gat gac tat	292
Thr Thr Glu Met Leu Gln Glu Trp Leu Ala Ala Val Gly Asp Asp Tyr	
80 85 90	
gct gct gtg gtc tgg agg cct gag ggc gag ccc agg ttc tac cca gat	340
Ala Ala Val Val Trp Arg Pro Glu Gly Glu Pro Arg Phe Tyr Pro Asp	
95 100 105	
gaa gag ggt ccc aag cac tgg acc aaa gaa agg cac cag ttt ctg atg	388
Glu Glu Gly Pro Lys His Trp Thr Lys Glu Arg His Gln Phe Leu Met	
110 115 120	
gag ctg aag cag gaa gcc ctc acc ttt gcc agg aac tgg ggg gcc gac	436
Glu Leu Lys Gln Glu Ala Leu Thr Phe Ala Arg Asn Trp Gly Ala Asp	
125 130 135	
tat atc ctg ttt gca gac aca gac aac att ctg acc aac aat cag act	484
Tyr Ile Leu Phe Ala Asp Thr Asp Asn Ile Leu Thr Asn Asn Gln Thr	
140 145 150 155	
ctg cgg ctt ctc atg ggg cag ggg ctt cca gtg gtg gcc cca atg ctg	532
Leu Arg Leu Leu Met Gly Gln Gly Leu Pro Val Val Ala Pro Met Leu	
160 165 170	
gac tcc cag acc tac tac tcc aac ttc tgg tgt ggg atc acc ccc cag	580
Asp Ser Gln Thr Tyr Tyr Ser Asn Phe Trp Cys Gly Ile Thr Pro Gln	
175 180 185	
ggc tac tac cgc cgc aca gcc gag tac ttc ccc acc aag aac cgc cag	628
Gly Tyr Tyr Arg Arg Thr Ala Glu Tyr Phe Pro Thr Lys Asn Arg Gln	
190 195 200	
cgc cgg ggc tgc ttc cgt gtc ccc atg gtc cac tcc acc ttc ctt gca	676
Arg Arg Gly Cys Phe Arg Val Pro Met Val His Ser Thr Phe Leu Ala	
205 210 215	
tcc ctg cgg gct gaa ggg gca gac cag ctt gct ttc tac ccg cca cat	724
Ser Leu Arg Ala Glu Gly Ala Asp Gln Leu Ala Phe Tyr Pro Pro His	

36/233

220	225	230	235	
ccc aac tac act tgg cct ttc gac gac atc atc gtc ttc gcc tat gcc				772
Pro Asn Tyr Thr Trp Pro Phe Asp Asp Ile Ile Val Phe Ala Tyr Ala				
	240	245	250	
tgc cag gct gct ggg gtc tcc gtc cac gtg tgc aat gag cac cgt tat				820
Cys Gln Ala Ala Gly Val Ser Val His Val Cys Asn Glu His Arg Tyr				
	255	260	265	
ggg tac atg aat gtg ccg gtg aaa tcc cac cag ggg ctg gaa gac gag				868
Gly Tyr Met Asn Val Pro Val Lys Ser His Gln Gly Leu Glu Asp Glu				
	270	275	280	
agg gtc aac ttc atc cac ctg atc tta gaa gca cta gtg gac ggc ccc				916
Arg Val Asn Phe Ile His Leu Ile Leu Glu Ala Leu Val Asp Gly Pro				
	285	290	295	
cgc atg cag gcc tca gct cat gtg act cgg ccc tct aag agg ccc agc				964
Arg Met Gln Ala Ser Ala His Val Thr Arg Pro Ser Lys Arg Pro Ser				
300	305	310	315	
aag ata ggg ttt gac gag gtc ttt gtc atc agc ctg gct cgc agg cct				1012
Lys Ile Gly Phe Asp Glu Val Phe Val Ile Ser Leu Ala Arg Arg Pro				
	320	325	330	
gac cgt cgg gaa cgc atg ctc gcc tcg ctc tgg gag atg gag atc tct				1060
Asp Arg Arg Glu Arg Met Leu Ala Ser Leu Trp Glu Met Glu Ile Ser				
	335	340	345	
ggg agg gtg gtg gac gct gtg gat ggc tgg atg ctc aac agc agt gcc				1108
Gly Arg Val Val Asp Ala Val Asp Gly Trp Met Leu Asn Ser Ser Ala				
	350	355	360	
atc agg aac ctc ggc gta gac ctg ctc ccg ggc tac cag gac cct tac				1156
Ile Arg Asn Leu Gly Val Asp Leu Leu Pro Gly Tyr Gln Asp Pro Tyr				
	365	370	375	
tcg ggc cgc act ctg acc aag ggc gag gtg ggc tgc ttc ctc agc cat				1204
Ser Gly Arg Thr Leu Thr Lys Gly Glu Val Gly Cys Phe Leu Ser His				
380	385	390	395	
tac tcc atc tgg gaa gag gtg gtt gcc agg ggc ctg gcc cgg gtc ctg				1252
Tyr Ser Ile Trp Glu Glu Val Val Ala Arg Gly Leu Ala Arg Val Leu				
	400	405	410	
gtg ttt gag gat gac gtg cgc ttt gag agc aac ttc agg ggg cgg ctg				1300

37/233

Val Phe Glu Asp Asp Val Arg Phe Glu Ser Asn Phe Arg Gly Arg Leu	
415 420 425	
gag cgg ctg atg gag gat gtg gag gca gag aaa ctg tct tgg gac ctg	1348
Glu Arg Leu Met Glu Asp Val Glu Ala Glu Lys Leu Ser Trp Asp Leu	
430 435 440	
atc tac ctc gga cgg aag cag gtg aac cct gag aag gag acg gcc gtg	1396
Ile Tyr Leu Gly Arg Lys Gln Val Asn Pro Glu Lys Glu Thr Ala Val	
445 450 455	
gag ggg ctg ccg ggc ctg gtg gtg gct ggg tac tcc tac tgg acg ctg	1444
Glu Gly Leu Pro Gly Leu Val Val Ala Gly Tyr Ser Tyr Trp Thr Leu	
460 465 470 475	
gcc tat gcc ctg cgt ctg gcg ggt gcc cgc aag ctg ctg gcc tca cag	1492
Ala Tyr Ala Leu Arg Leu Ala Gly Ala Arg Lys Leu Leu Ala Ser Gln	
480 485 490	
cct ctg cgc cgc atg ctg ccc gtg gac gag ttc ctg ccc atc atg ttc	1540
Pro Leu Arg Arg Met Leu Pro Val Asp Glu Phe Leu Pro Ile Met Phe	
495 500 505	
gac cag cac ccc aac gag cag tac aag gca cac ttc tgg cca cgg gac	1588
Asp Gln His Pro Asn Glu Gln Tyr Lys Ala His Phe Trp Pro Arg Asp	
510 515 520	
ctg gtg gcc ttc tcc gcc cag ccc ctg ctc gct gcc cct acc cac tat	1636
Leu Val Ala Phe Ser Ala Gln Pro Leu Leu Ala Ala Pro Thr His Tyr	
525 530 535	
gcc ggg gac gcc gag tgg ctc agt gac acg gag aca tcc tct cca tgg	1684
Ala Gly Asp Ala Glu Trp Leu Ser Asp Thr Glu Thr Ser Ser Pro Trp	
540 545 550 555	
gat gat gac agc ggc cgc ctc atc agc tgg agc ggc tcc caa aag acc	1732
Asp Asp Asp Ser Gly Arg Leu Ile Ser Trp Ser Gly Ser Gln Lys Thr	
560 565 570	
ctg cgc agc ccc cgc ctg gac ctg act ggc agc agc ggg cac agc ctc	1780
Leu Arg Ser Pro Arg Leu Asp Leu Thr Gly Ser Ser Gly His Ser Leu	
575 580 585	
caa ccc cag ccc cga gat gag ctc taggtccagg tgatgactgc aaagca	1830
Gln Pro Gln Pro Arg Asp Glu Leu	
590 595	

38/233

```

gtgtccagga gcaggccact actgcccaga gagcagagga ggaggttgtt ggcagggact 1890
gcagatcctg tcagacctgg ccaccacctt gggcatggcc actctgccct ctggacctgt 1950
ctttcatcgg gagaaaccac tcagagatgg atccatttcc ctaaaggctc cacagcaaag 2010
gagcaggact cccaggcccc tgtacctgc ctggcctgat tcagggcctt gtggccccc 2070
gcttctgttt caagctgggc agaccccagg atcccttccc tccctaagga ctcagctgag 2130
gggcccctct gccccttct acctccacct cagcaccctc cccagcttg atgtttgggt 2190
ctccccagca cctcctccc tggccggtgc aaagtacagg gaggtaaagc aggacccttg 2250
cagacatgtt gccagcaca cagtaggccc tcaataaaaag ccatttgcac tttaaatata 2310
tatatgtatg tatatatatg tatatatata tatatatata tatgt 2355

```

<210> 26

<211> 1024

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (27)...(821)

<400> 26

```

cggatggaag ctccggccgc ggagtg atg gtg gcc tca gcg aag atg ggc cgg 53
                               Met Val Ala Ser Ala Lys Met Gly Arg
                               1             5

gca ggg acc atg gcg gtg gca gca gag ctt cga gag ctg tgc cca gga 101
Ala Gly Thr Met Ala Val Ala Ala Glu Leu Arg Glu Leu Cys Pro Gly
 10             15             20             25

gtg aac aac cag ccc tac ctc tgt gag agt ggt cac tgc tgc ggg gag 149
Val Asn Asn Gln Pro Tyr Leu Cys Glu Ser Gly His Cys Cys Gly Glu
 30             35             40

act ggc tgc tgc acc tac tac tat gag ctc tgg tgg ttc tgg ctg ctc 197
Thr Gly Cys Cys Thr Tyr Tyr Tyr Glu Leu Trp Trp Phe Trp Leu Leu
 45             50             55

tgg act gtc ctc atc ctc ttt agc tgc tgt tgc gcc ttc cgc cac cga 245
Trp Thr Val Leu Ile Leu Phe Ser Cys Cys Cys Ala Phe Arg His Arg
 60             65             70

cga gct aaa ctc agg ctg caa caa cag cag cgg cag cgt gaa atc aac 293
Arg Ala Lys Leu Arg Leu Gln Gln Gln Gln Arg Gln Arg Glu Ile Asn

```

39/233

75	80	85	
ttg ttg gcc tat cat ggg gca tgc cat ggg gct ggt cct ttc cct acc			341
Leu Leu Ala Tyr His Gly Ala Cys His Gly Ala Gly Pro Phe Pro Thr			
90	95	100	105
ggt tca ctg ctt gac ctt cgc ttc ctc agc acc ttc aag ccc cca gcc			389
Gly Ser Leu Leu Asp Leu Arg Phe Leu Ser Thr Phe Lys Pro Pro Ala			
110	115	120	
tac gag gat gtg gtt cac cgc cca ggc aca cca ccc ccc cct tat act			437
Tyr Glu Asp Val Val His Arg Pro Gly Thr Pro Pro Pro Pro Tyr Thr			
125	130	135	
gtg gcc cca ggc cgc ccc ttg act gct tcc agt gaa caa acc tgc tgt			485
Val Ala Pro Gly Arg Pro Leu Thr Ala Ser Ser Glu Gln Thr Cys Cys			
140	145	150	
tcc tcc tca tcc agc tgc cct gcc cac ttt gaa gga aca aat gtg gaa			533
Ser Ser Ser Ser Ser Cys Pro Ala His Phe Glu Gly Thr Asn Val Glu			
155	160	165	
ggt gtt tcc tcc cac cag agt gcc ccc ccc cat cag gag ggt gag ccc			581
Gly Val Ser Ser His Gln Ser Ala Pro Pro His Gln Glu Gly Glu Pro			
170	175	180	185
ggg gca ggg gtg acc cct gcc tcc aca ccc ccc tcc tgc cgc tat cgc			629
Gly Ala Gly Val Thr Pro Ala Ser Thr Pro Pro Ser Cys Arg Tyr Arg			
190	195	200	
cgt tta act ggc gac tcc ggt att gag ctc tgc cct tgt cct gcc tcc			677
Arg Leu Thr Gly Asp Ser Gly Ile Glu Leu Cys Pro Cys Pro Ala Ser			
205	210	215	
ggt gag ggt gag cca gtc aag gag gtg agg gtt agt gcc acc ctg cca			725
Gly Glu Gly Glu Pro Val Lys Glu Val Arg Val Ser Ala Thr Leu Pro			
220	225	230	
gat ctg gag gac tac tcc ccg tgt gca cta ccc cca gag tct gta ccg			773
Asp Leu Glu Asp Tyr Ser Pro Cys Ala Leu Pro Pro Glu Ser Val Pro			
235	240	245	
cag atc ttt ccc atg ggg ctg tct tcc agt gaa ggg gac atc cca			818
Gln Ile Phe Pro Met Gly Leu Ser Ser Ser Glu Gly Asp Ile Pro			
250	255	260	
ta agtagttttg agaggggtgga tgggttactt gccaccaga aacagcccta			870

gtcccaactc cttgcgttcc tttggcccct ccctgcctac ctagaatctg cctgaaaggg 930
ctggagaggg gcagtattgg gggactgtgc tagctttacc cccgcaggac atacacagga 990
gcctttgata tcattaaaqa gatgtgaacc aqct 1024

tactggctac	tggcgctgca	gcc	atg	cag	ccc	ccg	ccc	ccg	ggc	ccg	ctg	ggc		53		
			Met	Gln	Pro	Pro	Pro	Pro	Gly	Pro	Leu	Gly				
			1					5					10			
gac	tgc	ctg	cgg	gac	tgg	gag	gat	cta	cag	cag	gac	ttc	cag	aac	atc	101
Asp	Cys	Leu	Arg	Asp	Trp	Glu	Asp	Leu	Gln	Gln	Asp	Phe	Gln	Asn	Ile	
			15					20					25			
cag	gag	acc	cat	cgg	ctc	tac	cgc	ctg	aag	ctg	gag	gag	ctg	acc	aaa	149
Gln	Glu	Thr	His	Arg	Leu	Tyr	Arg	Leu	Lys	Leu	Glu	Glu	Leu	Thr	Lys	
			30					35					40			
ctt	cag	aac	aat	tgc	acc	agc	tcc	atc	acg	cgg	cag	aag	aag	cgg	ctc	197
Leu	Gln	Asn	Asn	Cys	Thr	Ser	Ser	Ile	Thr	Arg	Gln	Lys	Lys	Arg	Leu	
			45					50					55			
cag	gag	ctg	gcc	ctc	gcc	ctg	aag	aaa	tgc	aaa	ccc	tcc	ctc	cca	gca	245
Gln	Glu	Leu	Ala	Leu	Ala	Leu	Lys	Lys	Cys	Lys	Pro	Ser	Leu	Pro	Ala	
			60					65					70			
gag	gcc	gag	ggg	gcc	gca	cag	gag	ctg	gag	aac	cag	atg	aaa	gag	cgc	293
Glu	Ala	Glu	Gly	Ala	Ala	Gln	Glu	Leu	Glu	Asn	Gln	Met	Lys	Glu	Arg	
			75					80					85		90	
caa	ggc	ctc	ttc	ttt	gac	atg	gag	gcc	tat	ttg	cct	aag	aag	aat	gga	341
Gln	Gly	Leu	Phe	Phe	Asp	Met	Glu	Ala	Tyr	Leu	Pro	Lys	Lys	Asn	Gly	
			95					100					105			
ttg	tac	ctg	agc	ctg	gtt	ctg	ggg	aac	gtc	aac	gtc	acg	ctc	ctg	agc	389
Leu	Tyr	Leu	Ser	Leu	Val	Leu	Gly	Asn	Val	Asn	Val	Thr	Leu	Leu	Ser	

41/233

110	115	120	
aag cag gct aag ttt gcc tac aag gac gag tat gag aag ttc aag ctc			437
Lys Gln Ala Lys Phe Ala Tyr Lys Asp Glu Tyr Glu Lys Phe Lys Leu			
125	130	135	
tac ctc acc atc atc ctc atc ctc atc tcc ttc act tgc cgc ttc ctg			485
Tyr Leu Thr Ile Ile Leu Ile Leu Ile Ser Phe Thr Cys Arg Phe Leu			
140	145	150	
ctc aac tcc agg gtg aca gat gct gcc ttc aac ttc ctg ctg gtc tgg			533
Leu Asn Ser Arg Val Thr Asp Ala Ala Phe Asn Phe Leu Leu Val Trp			
155	160	165	170
tac tac tgc acc ctg acc atc cgg gag agc atc ctc atc aac aac ggc			581
Tyr Tyr Cys Thr Leu Thr Ile Arg Glu Ser Ile Leu Ile Asn Asn Gly			
175	180	185	
tcc cgg atc aaa ggc tgg tgg gtg ttc cat cac tac gtg tcc acc ttc			629
Ser Arg Ile Lys Gly Trp Trp Val Phe His His Tyr Val Ser Thr Phe			
190	195	200	
ctg tgc gga gtc atg ctg acg tgg ccc gac ggt ctc atg tac cag aaa			677
Leu Ser Gly Val Met Leu Thr Trp Pro Asp Gly Leu Met Tyr Gln Lys			
205	210	215	
ttc cgg aac caa ttc ctc tcc ttt tcc atg tac cag agc ttc gtg cag			725
Phe Arg Asn Gln Phe Leu Ser Phe Ser Met Tyr Gln Ser Phe Val Gln			
220	225	230	
ttt ctc cag tac tac tac cag agc ggc tgc ctc tac cgc ctg cgg gcg			773
Phe Leu Gln Tyr Tyr Tyr Gln Ser Gly Cys Leu Tyr Arg Leu Arg Ala			
235	240	245	250
ctg ggc gag cgg cac acc atg gac ctc act gtg gag ggc ttc cag tcc			821
Leu Gly Glu Arg His Thr Met Asp Leu Thr Val Glu Gly Phe Gln Ser			
255	260	265	
tgg atg tgg cgg ggc ctc acc ttc ctg ctg cct ttt ctt ttc ttt gga			869
Trp Met Trp Arg Gly Leu Thr Phe Leu Leu Pro Phe Leu Phe Phe Gly			
270	275	280	
cac ttc tgg cag ctt ttt aac gcg ctg acg ttg ttc aac ctg gcc cag			917
His Phe Trp Gln Leu Phe Asn Ala Leu Thr Leu Phe Asn Leu Ala Gln			
285	290	295	
gac cct cag tgc aag gag tgg cag gtg ctt atg tgc ggc ttt ccc ttc			965

42/233

Asp Pro Gln Cys Lys Glu Trp Gln Val Leu Met Cys Gly Phe Pro Phe
 300 305 310
 ctc ctc ctt ttc ctc ggc aat ttc ttc acc acc ctg agg gtt gtg cac 1013
 Leu Leu Leu Phe Leu Gly Asn Phe Phe Thr Thr Leu Arg Val Val His
 315 320 325 330
 cac aag ttt cac agt cag cgg cac ggg agc aag aag gat tgaggctg 1060
 His Lys Phe His Ser Gln Arg His Gly Ser Lys Lys Asp
 335 340
 ggccttcccc tgccggccca gaggggcttc tgtcctgtgt gttgtgggag gggatgggag 1120
 gcgcccctcg agtgtgcgtg taccaggggg tctcttctat tctcccttgg gttttatggg 1180
 cgctgtgggc cctgaaggaa gacctggggc cagtgccttc aataaagaga ggcccag 1237

<210> 28
 <211> 1332
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (39)...(773)
 <400> 28

agtgcccccag cggaagcaca gctcagagct ggtctgcc atg gac atc ctg gtc cca 56
 Met Asp Ile Leu Val Pro
 1 5
 ctc ctg cag ctg ctg gtg ctg ctt ctt acc ctg ccc ctg cac ctc atg 104
 Leu Leu Gln Leu Leu Val Leu Leu Leu Thr Leu Pro Leu His Leu Met
 10 15 20
 gct ctg ctg ggc tgc tgg cag ccc ctg tgc aaa agc tac ttc ccc tac 152
 Ala Leu Leu Gly Cys Trp Gln Pro Leu Cys Lys Ser Tyr Phe Pro Tyr
 25 30 35
 ctg atg gcc gtg ctg act ccc aag agc aac cgc aag atg gag agc aag 200
 Leu Met Ala Val Leu Thr Pro Lys Ser Asn Arg Lys Met Glu Ser Lys
 40 45 50
 aaa cgg gag ctc ttc agc cag ata aag ggg ctt aca gga gcc tcc ggg 248
 Lys Arg Glu Leu Phe Ser Gln Ile Lys Gly Leu Thr Gly Ala Ser Gly
 55 60 65 70

43/233

aaa gtg gcc cta ctg gag ctg ggc tgc gga acc gga gcc aac ttt cag	296
Lys Val Ala Leu Leu Glu Leu Gly Cys Gly Thr Gly Ala Asn Phe Gln	
75 80 85	
ttc tac cca ccg ggc tgc agg gtc acc tgc cta gac cca aat ccc cac	344
Phe Tyr Pro Pro Gly Cys Arg Val Thr Cys Leu Asp Pro Asn Pro His	
90 95 100	
ttt gag aag ttc ctg aca aag agc atg gct gag aac agg cac ctc caa	392
Phe Glu Lys Phe Leu Thr Lys Ser Met Ala Glu Asn Arg His Leu Gln	
105 110 115	
tat gag cgg ttt gtg gtg gct cct gga gag gac atg aga cag ctg gct	440
Tyr Glu Arg Phe Val Val Ala Pro Gly Glu Asp Met Arg Gln Leu Ala	
120 125 130	
gat ggc tcc atg gat gtg gtg gtc tgc act ctg gtg ctg tgc tct gtg	488
Asp Gly Ser Met Asp Val Val Val Cys Thr Leu Val Leu Cys Ser Val	
135 140 145 150	
cag agc cca agg aag gtc ctg cag gag gtc cgg aga gta ctg aga ccg	536
Gln Ser Pro Arg Lys Val Leu Gln Glu Val Arg Arg Val Leu Arg Pro	
155 160 165	
gga ggt gtg ctc ttt ttc tgg gag cat gtg gca gaa cca tat gga agc	584
Gly Gly Val Leu Phe Phe Trp Glu His Val Ala Glu Pro Tyr Gly Ser	
170 175 180	
tgg gcc ttc atg tgg cag caa gtt ttc gag ccc acc tgg aaa cac att	632
Trp Ala Phe Met Trp Gln Gln Val Phe Glu Pro Thr Trp Lys His Ile	
185 190 195	
ggg gat ggc tgc tgc ctc acc aga gag acc tgg aag gat ctt gag aac	680
Gly Asp Gly Cys Cys Leu Thr Arg Glu Thr Trp Lys Asp Leu Glu Asn	
200 205 210	
gcc cag ttc tcc gaa atc caa atg gaa cga cag ccc cct ccc ttg aag	728
Ala Gln Phe Ser Glu Ile Gln Met Glu Arg Gln Pro Pro Pro Leu Lys	
215 220 225 230	
tgg cta cct gtt ggg ccc cac atc atg gga aag gct gtc aaa taatcttcc	780
Trp Leu Pro Val Gly Pro His Ile Met Gly Lys Ala Val Lys	
235 240	
caagctccaa ggcactcatt tgctccttcc ccagcctcca attagaacaa gccacccacc	840
agcctatcta tottccactg agagggacct agcagaatga gagaagacat tcatgtacca	900

cctactagtc	cctctctccc	caacctctgc	cagggcaatc	tctaaactca	atcccgcctt	960
cgacagtga	aaagctctac	ttctacgctg	acccaggagg	gaaacactag	gacctgtgtg	1020
tatcctcaac	tgcaagtttc	tggactagtc	tcccaacggt	tgctctccaa	tgttgctccct	1080
ttccttcgtt	cccatggtaa	agctcctctc	gctttcctcc	tgaggctaca	cccatgcgtc	1140
tctaggaact	ggtcacaaaa	gtcatgggtc	ctgcatecct	gccaaagccc	cctgaccctc	1200
tctccccact	accaccttct	tcttgagctg	ggggcaccag	ggagaatcag	agatgctggg	1260
gatgccagag	caagactcaa	agaggcagag	gttttgttct	caaatatattt	ttaataaata	1320
gacgaaacca	cq					1332

agaccccgcc tgctcgggcg cgggcggcgg cgcggcc atg aag ctg aag ctg aag 55
Met Lys Leu Lys Leu Lys

1 5

10 15 20

25 30 35

40 45 50

55 60 65 70

75 80 85

45/233

ccc ctg tgg gtg cag tac cct cag gat gtg act acc ttc aat ata gat	343
Pro Leu Trp Val Gln Tyr Pro Gln Asp Val Thr Thr Phe Asn Ile Asp	
90 95 100	
gat cag tac ttg ctt ggg gat gcg ttg ctg gtt cac cct gta tca gac	391
Asp Gln Tyr Leu Leu Gly Asp Ala Leu Leu Val His Pro Val Ser Asp	
105 110 115	
tct gga gcc cat ggt gtc cag gtc tat ctg cct ggc caa ggg gag gtg	439
Ser Gly Ala His Gly Val Gln Val Tyr Leu Pro Gly Gln Gly Glu Val	
120 125 130	
tgg tat gac att caa agc tac cag aag cat cat ggt ccc cag acc ctg	487
Trp Tyr Asp Ile Gln Ser Tyr Gln Lys His His Gly Pro Gln Thr Leu	
135 140 145 150	
tac ctg cct gta act cta agc agt atc cct gtg ttc cag cgt gga ggg	535
Tyr Leu Pro Val Thr Leu Ser Ser Ile Pro Val Phe Gln Arg Gly Gly	
155 160 165	
aca atc gtg cct cga tgg atg cga gtg cgg cgg tct tca gaa tgt atg	583
Thr Ile Val Pro Arg Trp Met Arg Val Arg Arg Ser Ser Glu Cys Met	
170 175 180	
aag gat gac ccc atc act ctc ttt gtt gca ctt agc cct cag ggt aca	631
Lys Asp Asp Pro Ile Thr Leu Phe Val Ala Leu Ser Pro Gln Gly Thr	
185 190 195	
gct caa gga gag ctc ttt ctg gat gat ggg cac acg ttc aac tat cag	679
Ala Gln Gly Glu Leu Phe Leu Asp Asp Gly His Thr Phe Asn Tyr Gln	
200 205 210	
act cgc caa gag ttc ctg ctg cgt cga ttc tca ttc tct ggc aac acc	727
Thr Arg Gln Glu Phe Leu Leu Arg Arg Phe Ser Phe Ser Gly Asn Thr	
215 220 225 230	
ctt gtc tcc agc tca gca gac cct gaa gga cac ttt gag aca cca atc	775
Leu Val Ser Ser Ser Ala Asp Pro Glu Gly His Phe Glu Thr Pro Ile	
235 240 245	
tgg att gag cgg gtg gtg ata ata ggg gct gga aag cca gca gct gtg	823
Trp Ile Glu Arg Val Val Ile Ile Gly Ala Gly Lys Pro Ala Ala Val	
250 255 260	
gta ctc cag aca aaa gga tct cca gaa agc cgc ctg tcc ttc cag cat	871
Val Leu Gln Thr Lys Gly Ser Pro Glu Ser Arg Leu Ser Phe Gln His	

46/233

265	270	275	
gac cct gag acc tct gtg ttg gtc ctg cgc aag cct ggc atc aat gtg			919
Asp Pro Glu Thr Ser Val Leu Val Leu Arg Lys Pro Gly Ile Asn Val			
280	285	290	
gca tct gat tgg agt att cac ctg cga taacccaagg gatgttctgg gtta			970
Ala Ser Asp Trp Ser Ile His Leu Arg			
295	300		
gggggagggga aggggagcat tagtgetgag agatattcct tcttctgcct tggagtctgg			1030
ccctccccag acttcaactta tgctagtcta agaccagat tctgccaaca tttgggcagg			1090
atgagagggc tgaccctggg ctocaaatct ctcttgtgat ctctcacct ctcccaactcc			1150
attgatacca actctttccc ttcattcccc caacatcctg ttgtctaac tggagcacat			1210
tcacttacga acaccaggaa accacagggc ccttgctgcc ccttctcttt cccttattta			1270
ggagccctga actccccag agtctatcca ttcattgcctc ttgtatgttg atgccacttc			1330
ttggaagaag atgagggcaa tgagttaggg ctcttttccc ccttccctcc caccagattg			1390
ctctccccacc tttcatttct tctccaggc tttactcccc tttttatgcc ccaccgatac			1450
actgggacca ccccttacc cggacaggat gaatggatca aaggagttag gttgctaaag			1510
aacatccttt tccctctcat tctacccttt tctctcccc gattccttgt agagctgctg			1570
caattcttag aggggcagtt ctacctctc tgtccctcgg cagaaagacg tttccacacc			1630
tcttagggga tgcgcattaa acttcttttg ccccttctt gtccctttg aggggcactt			1690
aagatggaga aatcagttgt ggtttcagtg aatcatggtc acctgtattt attgctagga			1750
gaagcctgag ggtgggggga gatgatcatg tgtgctcggg gttggctgga agccctgggt			1810
gggggggttg gggaggacta atggggagtc ggggaatatt tgtgggtatt ttttttactt			1870
cctcttggtt cccagctgtg acacgttttg atcaaaggag aaacaataaa gggataaacc			1930
at			1932

<210> 30

<211> 1124

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (73)...(555)

<400> 30

ggaagagccg tcaacttagc gagcgcaaca ggctgccgct gaggagctgg agctgggtggg	60
gactggggccg ca atg gac aag ctg aag aag gtg ctg agc ggg cag gac acg	111

47/233

Met Asp Lys Leu Lys Lys Val Leu Ser Gly Gln Asp Thr									
1		5		10					
gag gac cgg agc ggc ctg tcc gag gtt gtt gag gca tct tca tta agc						159			
Glu Asp Arg Ser Gly Leu Ser Glu Val Val Glu Ala Ser Ser Leu Ser									
15		20		25					
tgg agt acc agg ata aaa ggc ttc att gcg tgt ttt gct ata gga att						207			
Trp Ser Thr Arg Ile Lys Gly Phe Ile Ala Cys Phe Ala Ile Gly Ile									
30		35		40		45			
ctc tgc tca ctg ctg ggt act gtt ctg ctg tgg gtg ccc agg aag gga						255			
Leu Cys Ser Leu Leu Gly Thr Val Leu Leu Trp Val Pro Arg Lys Gly									
50		55		60					
cta cac ctc ttc gca gtg ttt tat acc ttt ggt aat atc gca tca att						303			
Leu His Leu Phe Ala Val Phe Tyr Thr Phe Gly Asn Ile Ala Ser Ile									
65		70		75					
ggg agt acc atc ttc ctc atg gga cca gtg aaa cag ctg aag cga atg						351			
Gly Ser Thr Ile Phe Leu Met Gly Pro Val Lys Gln Leu Lys Arg Met									
80		85		90					
ttt gag cct act cgt ttg att gca act atc atg gtg ctg ttg tgt ttt						399			
Phe Glu Pro Thr Arg Leu Ile Ala Thr Ile Met Val Leu Leu Cys Phe									
95		100		105					
gca ctt acc ctg tgt tct gcc ttt tgg tgg cat aac aag gga ctt gca						447			
Ala Leu Thr Leu Cys Ser Ala Phe Trp Trp His Asn Lys Gly Leu Ala									
110		115		120		125			
ctt atc ttc tgc att ttg cag tct ttg gca ttg acg tgg tac agc ctt						495			
Leu Ile Phe Cys Ile Leu Gln Ser Leu Ala Leu Thr Trp Tyr Ser Leu									
130		135		140					
tcc ttc ata cca ttt gca agg gat gct gtg aag aag tgt ttt gcc gtg						543			
Ser Phe Ile Pro Phe Ala Arg Asp Ala Val Lys Lys Cys Phe Ala Val									
145		150		155					
tgt ctt gca taattcatgg ccagttttat gaagctttgg aaggcactat ggacagaa						600			
Cys Leu Ala									
160									
gctggtggac agttttgtaa ctatcttcga aacctctgtc ttacagacat gtgcctttta						660			
tcttgacagca atgtgttgct tgtgattcga acatttgagg gttacttttg gaagcaacaa						720			
tacattctcg aacctgaatg tcagtagcac aggatgagaa gtgggttctg tatcttgtgg						780			

48/233

```

agtggaaatct tctcatgta cctgtttcct ctctggatgt tgtccactg aattcccatg      840
aatacaaacc tattcagcaa cagcacataa gccttgggtg caagtgattc ccaggtggca      900
aaaggcagcc ccatcagaga tcacgggagc aacagtaagg gacagagttt tgggggtccac      960
ttgtccctca gcatggaagc catcacctg gtctgcata gagtgagtct acttctactc     1020
tggcatctga gaacaagtga ctctgcttta gacaagcccc tggagagcct ggccatggag     1080
tgaggtagaa aagaagcact ttttggtggt atatgctgtt tctg                      1124

```

<210> 31

<211> 1445

<212> PRT

<213> Homo sapiens

<400> 31

```

Met Gln Gly Pro Pro Leu Leu Thr Ala Ala His Leu Leu Cys Val Cys
  1              5              10              15
Thr Ala Ala Leu Ala Val Ala Pro Gly Pro Arg Phe Leu Val Thr Ala
      20              25              30
Pro Gly Ile Ile Arg Pro Gly Gly Asn Val Thr Ile Gly Val Glu Leu
      35              40              45
Leu Glu His Cys Pro Ser Gln Val Thr Val Lys Ala Glu Leu Leu Lys
      50              55              60
Thr Ala Ser Asn Leu Thr Val Ser Val Leu Glu Ala Glu Gly Val Phe
      65              70              75              80
Glu Lys Gly Ser Phe Lys Thr Leu Thr Leu Pro Ser Leu Pro Leu Asn
      85              90              95
Ser Ala Asp Glu Ile Tyr Glu Leu Arg Val Thr Gly Arg Thr Gln Asp
      100             105             110
Glu Ile Leu Phe Ser Asn Ser Thr Arg Leu Ser Phe Glu Thr Lys Arg
      115             120             125
Ile Ser Val Phe Ile Gln Thr Asp Lys Ala Leu Tyr Lys Pro Lys Gln
      130             135             140
Glu Val Lys Phe Arg Ile Val Thr Leu Phe Ser Asp Phe Lys Pro Tyr
      145             150             155             160
Lys Thr Ser Leu Asn Ile Leu Ile Lys Asp Pro Lys Ser Asn Leu Ile
      165             170             175
Gln Gln Trp Leu Ser Gln Gln Ser Asp Leu Gly Val Ile Ser Lys Thr

```

49/233

180	185	190
Phe Gln Leu Ser Ser His Pro Ile Leu Gly Asp Trp Ser Ile Gln Val		
195	200	205
Gln Val Asn Asp Gln Thr Tyr Tyr Gln Ser Phe Gln Val Ser Glu Tyr		
210	215	220
Val Leu Pro Lys Phe Glu Val Thr Leu Gln Thr Pro Leu Tyr Cys Ser		
225	230	235
Met Asn Ser Lys His Leu Asn Gly Thr Ile Thr Ala Lys Tyr Thr Tyr		
245	250	255
Gly Lys Pro Val Lys Gly Asp Val Thr Leu Thr Phe Leu Pro Leu Ser		
260	265	270
Phe Trp Gly Lys Lys Lys Asn Ile Thr Lys Thr Phe Lys Ile Asn Gly		
275	280	285
Ser Ala Asn Phe Ser Phe Asn Asp Glu Glu Met Lys Asn Val Met Asp		
290	295	300
Ser Ser Asn Gly Leu Ser Glu Tyr Leu Asp Leu Ser Phe Pro Gly Pro		
305	310	315
Val Glu Ile Leu Thr Thr Val Thr Glu Ser Val Thr Gly Ile Ser Arg		
325	330	335
Asn Val Ser Thr Asn Val Phe Phe Lys Gln His Asp Tyr Ile Ile Glu		
340	345	350
Phe Phe Asp Tyr Thr Thr Val Leu Lys Pro Ser Leu Asn Phe Thr Ala		
355	360	365
Thr Val Lys Val Thr Arg Ala Asp Gly Asn Gln Leu Thr Leu Glu Glu		
370	375	380
Arg Arg Asn Asn Val Val Ile Thr Val Thr Gln Arg Asn Tyr Thr Glu		
385	390	395
Tyr Trp Ser Gly Ser Asn Ser Gly Asn Gln Lys Met Glu Ala Val Gln		
405	410	415
Lys Ile Asn Tyr Thr Val Pro Gln Ser Gly Thr Phe Lys Ile Glu Phe		
420	425	430
Pro Ile Leu Glu Asp Ser Ser Glu Leu Gln Leu Lys Ala Tyr Phe Leu		
435	440	445
Gly Ser Lys Ser Ser Met Ala Val His Ser Leu Phe Lys Ser Pro Ser		
450	455	460

50/233

Lys Thr Tyr Ile Gln Leu Lys Thr Arg Asp Glu Asn Ile Lys Val Gly
 465 470 475 480
 Ser Pro Phe Glu Leu Val Val Ser Gly Asn Lys Arg Leu Lys Glu Leu
 485 490 495
 Ser Tyr Met Val Val Ser Arg Gly Gln Leu Val Ala Val Gly Lys Gln
 500 505 510
 Asn Ser Thr Met Phe Ser Leu Thr Pro Glu Asn Ser Trp Thr Pro Lys
 515 520 525
 Ala Cys Val Ile Val Tyr Tyr Ile Glu Asp Asp Gly Glu Ile Ile Ser
 530 535 540
 Asp Val Leu Lys Ile Pro Val Gln Leu Val Phe Lys Asn Lys Ile Lys
 545 550 555 560
 Leu Tyr Trp Ser Lys Val Lys Ala Glu Pro Ser Glu Lys Val Ser Leu
 565 570 575
 Arg Ile Ser Val Thr Gln Pro Asp Ser Ile Val Gly Ile Val Ala Val
 580 585 590
 Asp Lys Ser Val Asn Leu Met Asn Ala Ser Asn Asp Ile Thr Met Glu
 595 600 605
 Asn Val Val His Glu Leu Glu Leu Tyr Asn Thr Gly Tyr Tyr Leu Gly
 610 615 620
 Met Phe Met Asn Ser Phe Ala Val Phe Gln Glu Cys Gly Leu Trp Val
 625 630 635 640
 Leu Thr Asp Ala Asn Leu Thr Lys Asp Tyr Ile Asp Gly Val Tyr Asp
 645 650 655
 Asn Ala Glu Tyr Ala Glu Arg Phe Met Glu Glu Asn Glu Gly His Ile
 660 665 670
 Val Asp Ile His Asp Phe Ser Leu Gly Ser Ser Pro His Val Arg Lys
 675 680 685
 His Phe Pro Glu Thr Trp Ile Trp Leu Asp Thr Asn Met Gly Ser Arg
 690 695 700
 Ile Tyr Gln Glu Phe Glu Val Thr Val Pro Asp Ser Ile Thr Ser Trp
 705 710 715 720
 Val Ala Thr Gly Phe Val Ile Ser Glu Asp Leu Gly Leu Gly Leu Thr
 725 730 735
 Thr Thr Pro Val Glu Leu Gln Ala Phe Gln Pro Phe Phe Ile Phe Leu

51/233

740	745	750
Asn Leu Pro Tyr Ser Val Ile Arg Gly Glu Glu Phe Ala Leu Glu Ile		
755	760	765
Thr Ile Phe Asn Tyr Leu Lys Asp Ala Thr Glu Val Lys Val Ile Ile		
770	775	780
Glu Lys Ser Asp Lys Phe Asp Ile Leu Met Thr Ser Ser Glu Ile Asn		
785	790	795
Ala Thr Gly His Gln Gln Thr Leu Leu Val Pro Ser Glu Asp Gly Ala		
805	810	815
Thr Val Leu Phe Pro Ile Arg Pro Thr His Leu Gly Glu Ile Pro Ile		
820	825	830
Thr Val Thr Ala Leu Ser Pro Thr Ala Ser Asp Ala Ile Thr Gln Met		
835	840	845
Ile Leu Val Lys Ala Glu Gly Ile Glu Lys Ser Tyr Ser Gln Ser Ile		
850	855	860
Leu Leu Asp Leu Thr Asp Asn Arg Leu Gln Ser Thr Leu Lys Thr Leu		
865	870	875
Ser Phe Ser Phe Pro Pro Asn Thr Val Thr Gly Ser Glu Arg Val Gln		
885	890	895
Ile Thr Ala Ile Gly Asp Val Leu Gly Pro Ser Ile Asn Gly Leu Ala		
900	905	910
Ser Leu Ile Arg Met Pro Tyr Gly Cys Gly Glu Gln Asn Met Ile Asn		
915	920	925
Phe Ala Pro Asn Ile Tyr Ile Leu Asp Tyr Leu Thr Lys Lys Lys Gln		
930	935	940
Leu Thr Asp Asn Leu Lys Glu Lys Ala Leu Ser Phe Met Arg Gln Gly		
945	950	955
Tyr Gln Arg Glu Leu Leu Tyr Gln Arg Glu Asp Gly Ser Phe Ser Ala		
965	970	975
Phe Gly Asn Tyr Asp Pro Ser Gly Ser Thr Trp Leu Ser Ala Phe Val		
980	985	990
Leu Arg Cys Phe Leu Glu Ala Asp Pro Tyr Ile Asp Ile Asp Gln Asn		
995	1000	1005
Val Leu His Arg Thr Tyr Thr Trp Leu Lys Gly His Gln Lys Ser Asn		
1010	1015	1020

52/233

Gly Glu Phe Trp Asp Pro Gly Arg Val Ile His Ser Glu Leu Gln Gly
 1025 1030 1035 1040
 Gly Asn Lys Ser Pro Val Thr Leu Thr Ala Tyr Ile Val Thr Ser Leu
 1045 1050 1055
 Leu Gly Tyr Arg Lys Tyr Gln Pro Asn Ile Asp Val Gln Glu Ser Ile
 1060 1065 1070
 His Phe Leu Glu Ser Glu Phe Ser Arg Gly Ile Ser Asp Asn Tyr Thr
 1075 1080 1085
 Leu Ala Leu Ile Thr Tyr Ala Leu Ser Ser Val Gly Ser Pro Lys Ala
 1090 1095 1100
 Lys Glu Ala Leu Asn Met Leu Thr Trp Arg Ala Glu Gln Glu Gly Gly
 1105 1110 1115 1120
 Met Gln Phe Trp Val Ser Ser Glu Ser Lys Leu Ser Asp Ser Trp Gln
 1125 1130 1135
 Pro Arg Ser Leu Asp Ile Glu Val Ala Ala Tyr Ala Leu Leu Ser His
 1140 1145 1150
 Phe Leu Gln Phe Gln Thr Ser Glu Gly Ile Pro Ile Met Arg Trp Leu
 1155 1160 1165
 Ser Arg Gln Arg Asn Ser Leu Gly Gly Phe Ala Ser Thr Gln Asp Thr
 1170 1175 1180
 Thr Val Ala Leu Lys Ala Leu Ser Glu Phe Ala Ala Leu Met Asn Thr
 1185 1190 1195 1200
 Glu Arg Thr Asn Ile Gln Val Thr Val Thr Gly Pro Ser Ser Pro Ser
 1205 1210 1215
 Pro Val Lys Phe Leu Ile Asp Thr His Asn Arg Leu Leu Leu Gln Thr
 1220 1225 1230
 Ala Glu Leu Ala Val Val Gln Pro Thr Ala Val Asn Ile Ser Ala Asn
 1235 1240 1245
 Gly Phe Gly Phe Ala Ile Cys Gln Leu Asn Val Val Tyr Asn Val Lys
 1250 1255 1260
 Ala Ser Gly Ser Ser Arg Arg Arg Arg Ser Ile Gln Asn Gln Glu Ala
 1265 1270 1275 1280
 Phe Asp Leu Asp Val Ala Val Lys Glu Asn Lys Asp Asp Leu Asn His
 1285 1290 1295
 Val Asp Leu Asn Val Cys Thr Ser Phe Ser Gly Pro Gly Arg Ser Gly

53/233

1300	1305	1310
Met Ala Leu Met Glu Val Asn Leu Leu Ser Gly Phe Met Val Pro Ser		
1315	1320	1325
Glu Ala Ile Ser Leu Ser Glu Thr Val Lys Lys Val Glu Tyr Asp His		
1330	1335	1340
Gly Lys Leu Asn Leu Tyr Leu Asp Ser Val Asn Glu Thr Gln Phe Cys		
1345	1350	1355
Val Asn Ile Pro Ala Val Arg Asn Phe Lys Val Ser Asn Thr Gln Asp		
1365	1370	1375
Ala Ser Val Ser Ile Val Asp Tyr Tyr Glu Pro Arg Arg Gln Ala Val		
1380	1385	1390
Arg Ser Tyr Asn Ser Glu Val Lys Leu Ser Ser Cys Asp Leu Cys Ser		
1395	1400	1405
Asp Val Gln Gly Cys Arg Pro Cys Glu Asp Gly Ala Ser Gly Ser His		
1410	1415	1420
His His Ser Ser Val Ile Phe Ile Phe Cys Phe Lys Leu Leu Tyr Phe		
1425	1430	1435
Met Glu Leu Trp Leu		1440
1445		

<210> 32

<211> 582

<212> PRT

<213> Homo sapiens

<400> 32

Met Phe Pro Ala Gly Pro Pro Ser His Ser Leu Leu Arg Leu Pro Leu
1 5 10 15
Leu Gln Leu Leu Leu Val Val Gln Ala Val Gly Arg Gly Leu Gly
20 25 30
Arg Ala Ser Pro Ala Gly Gly Pro Leu Glu Asp Val Val Ile Glu Arg
35 40 45
Tyr His Ile Pro Arg Ala Cys Pro Arg Glu Val Gln Met Gly Asp Phe
50 55 60
Val Arg Tyr His Tyr Asn Gly Thr Phe Glu Asp Gly Lys Lys Phe Asp
65 70 75 80

54/233

Ser Ser Tyr Asp Arg Asn Thr Leu Val Ala Ile Val Val Gly Val Gly
 85 90 95
 Arg Leu Ile Thr Gly Met Asp Arg Gly Leu Met Gly Met Cys Val Asn
 100 105 110
 Glu Arg Arg Arg Leu Ile Val Pro Pro His Leu Gly Tyr Gly Ser Ile
 115 120 125
 Gly Leu Ala Gly Leu Ile Pro Pro Asp Ala Thr Leu Tyr Phe Asp Val
 130 135 140
 Val Leu Leu Asp Val Trp Asn Lys Glu Asp Thr Val Gln Val Ser Thr
 145 150 155 160
 Leu Leu Arg Pro Pro His Cys Pro Arg Met Val Gln Asp Gly Asp Phe
 165 170 175
 Val Arg Tyr His Tyr Asn Gly Thr Leu Leu Asp Gly Thr Ser Phe Asp
 180 185 190
 Thr Ser Tyr Ser Lys Gly Gly Thr Tyr Asp Thr Tyr Val Gly Ser Gly
 195 200 205
 Trp Leu Ile Lys Gly Met Asp Gln Gly Leu Leu Gly Met Cys Pro Gly
 210 215 220
 Glu Arg Arg Lys Ile Ile Ile Pro Pro Phe Leu Ala Tyr Gly Glu Lys
 225 230 235 240
 Gly Tyr Gly Thr Val Ile Pro Pro Gln Ala Ser Leu Val Phe His Val
 245 250 255
 Leu Leu Ile Asp Val His Asn Pro Lys Asp Ala Val Gln Leu Glu Thr
 260 265 270
 Leu Glu Leu Pro Pro Gly Cys Val Arg Arg Ala Gly Ala Gly Asp Phe
 275 280 285
 Met Arg Tyr His Tyr Asn Gly Ser Leu Met Asp Gly Thr Leu Phe Asp
 290 295 300
 Ser Ser Tyr Ser Arg Asn His Thr Tyr Asn Thr Tyr Ile Gly Gln Gly
 305 310 315 320
 Tyr Ile Ile Pro Gly Met Asp Gln Gly Leu Gln Gly Ala Cys Met Gly
 325 330 335
 Glu Arg Arg Arg Ile Thr Ile Pro Pro His Leu Ala Tyr Gly Glu Asn
 340 345 350
 Gly Thr Gly Asp Lys Ile Pro Gly Ser Ala Val Leu Ile Phe Asn Val

55/233

355	360	365
His Val Ile Asp Phe His Asn Pro Ala Asp Val Val Glu Ile Arg Thr		
370	375	380
Leu Ser Arg Pro Ser Glu Thr Cys Asn Glu Thr Thr Lys Leu Gly Asp		
385	390	395
Phe Val Arg Tyr His Tyr Asn Cys Ser Leu Leu Asp Gly Thr Gln Leu		
405	410	415
Phe Thr Ser His Asp Tyr Gly Ala Pro Gln Glu Ala Thr Leu Gly Ala		
420	425	430
Asn Lys Val Ile Glu Gly Leu Asp Thr Gly Leu Gln Gly Met Cys Val		
435	440	445
Gly Glu Arg Arg Gln Leu Ile Val Pro Pro His Leu Ala His Gly Glu		
450	455	460
Ser Gly Ala Arg Gly Val Pro Gly Ser Ala Val Leu Leu Phe Glu Val		
465	470	475
Glu Leu Val Ser Arg Glu Asp Gly Leu Pro Thr Gly Tyr Leu Phe Val		
485	490	495
Trp His Lys Asp Pro Pro Ala Asn Leu Phe Glu Asp Met Asp Leu Asn		
500	505	510
Lys Asp Gly Glu Val Pro Pro Glu Glu Phe Ser Thr Phe Ile Lys Ala		
515	520	525
Gln Val Ser Glu Gly Lys Gly Arg Leu Met Pro Gly Gln Asp Pro Glu		
530	535	540
Lys Thr Ile Gly Asp Met Phe Gln Asn Gln Asp Arg Asn Gln Asp Gly		
545	550	555
Lys Ile Thr Val Asp Glu Leu Lys Leu Lys Ser Asp Glu Asp Glu Glu		
565	570	575
Arg Val His Glu Glu Leu		
580		

<210> 33

<211> 410

<212> PRT

<213> Homo sapiens

<400> 33

56/233

Met Glu Leu Pro Ser Gly Pro Gly Pro Glu Arg Leu Phe Asp Ser His
 1 5 10 15
 Arg Leu Pro Gly Asp Cys Phe Leu Leu Leu Val Leu Leu Leu Tyr Ala
 20 25 30
 Pro Val Gly Phe Cys Leu Leu Val Leu Arg Leu Phe Leu Gly Ile His
 35 40 45
 Val Phe Leu Val Ser Cys Ala Leu Pro Asp Ser Val Leu Arg Arg Phe
 50 55 60
 Val Val Arg Thr Met Cys Ala Val Leu Gly Leu Val Ala Arg Gln Glu
 65 70 75 80
 Asp Ser Gly Leu Arg Asp His Ser Val Arg Val Leu Ile Ser Asn His
 85 90 95
 Val Thr Pro Phe Asp His Asn Ile Val Asn Leu Leu Thr Thr Cys Ser
 100 105 110
 Thr Pro Leu Leu Asn Ser Pro Pro Ser Phe Val Cys Trp Ser Arg Gly
 115 120 125
 Phe Met Glu Met Asn Gly Arg Gly Glu Leu Val Glu Ser Leu Lys Arg
 130 135 140
 Phe Cys Ala Ser Thr Arg Leu Pro Pro Thr Pro Leu Leu Leu Phe Pro
 145 150 155 160
 Glu Glu Glu Ala Thr Asn Gly Arg Glu Gly Leu Leu Arg Phe Ser Ser
 165 170 175
 Trp Pro Phe Ser Ile Gln Asp Val Val Gln Pro Leu Thr Leu Gln Val
 180 185 190
 Gln Arg Pro Leu Val Ser Val Thr Val Ser Asp Ala Ser Trp Val Ser
 195 200 205
 Glu Leu Leu Trp Ser Leu Phe Val Pro Phe Thr Val Tyr Gln Val Arg
 210 215 220
 Trp Leu Arg Pro Val His Arg Gln Leu Gly Glu Ala Asn Glu Glu Phe
 225 230 235 240
 Ala Leu Arg Val Gln Gln Leu Val Ala Lys Glu Leu Gly Gln Thr Gly
 245 250 255
 Thr Arg Leu Thr Pro Ala Asp Lys Ala Glu His Met Lys Arg Gln Arg
 260 265 270
 His Pro Arg Leu Arg Pro Gln Ser Ala Gln Ser Ser Phe Pro Pro Ser

57/233

275	280	285
Pro Gly Pro Ser Pro Asp Val	Gln Leu Ala Thr Leu Ala Gln Arg Val	
290	295	300
Lys Glu Val Leu Pro His Val	Pro Leu Gly Val Ile Gln Arg Asp Leu	
305	310	315
Ala Lys Thr Gly Cys Val Asp	Leu Thr Ile Thr Asn Leu Leu Glu Gly	
325	330	335
Ala Val Ala Phe Met Pro Glu	Asp Ile Thr Lys Gly Thr Gln Ser Leu	
340	345	350
Pro Thr Ala Ser Ala Ser Lys	Phe Pro Ser Ser Gly Pro Val Thr Pro	
355	360	365
Gln Pro Thr Ala Leu Thr Phe	Ala Lys Ser Ser Trp Ala Arg Gln Glu	
370	375	380
Ser Leu Gln Glu Arg Lys Gln	Ala Leu Tyr Glu Tyr Ala Arg Arg Arg	
385	390	395
Phe Thr Glu Arg Arg Ala Gln	Glu Ala Asp	
405	410	

<210> 34

<211> 483

<212> PRT

<213> Homo sapiens

<400> 34

Met Glu Glu Gly Gly Gly Val	Arg Ser Leu Val Pro Gly Gly Pro
1	5 10 15
Val Leu Leu Val Leu Cys Gly	Leu Leu Glu Ala Ser Gly Gly Gly Arg
20	25 30
Ala Leu Pro Gln Leu Ser Asp	Asp Ile Pro Phe Arg Val Asn Trp Pro
35	40 45
Gly Thr Glu Phe Ser Leu Pro	Thr Thr Gly Val Leu Tyr Lys Glu Asp
50	55 60
Asn Tyr Val Ile Met Thr Thr	Ala His Lys Glu Lys Tyr Lys Cys Ile
65	70 75 80
Leu Pro Leu Val Thr Ser Gly	Asp Glu Glu Glu Lys Asp Tyr Lys
85	90 95

58/233

Gly Pro Asn Pro Arg Glu Leu Leu Glu Pro Leu Phe Lys Gln Ser Ser
 100 105 110
 Cys Ser Tyr Arg Ile Glu Ser Tyr Trp Thr Tyr Glu Val Cys His Gly
 115 120 125
 Lys His Ile Arg Gln Tyr His Glu Glu Lys Glu Thr Gly Gln Lys Ile
 130 135 140
 Asn Ile His Glu Tyr Tyr Leu Gly Asn Met Leu Ala Lys Asn Leu Leu
 145 150 155 160
 Phe Glu Lys Glu Arg Glu Ala Glu Glu Lys Glu Lys Ser Asn Glu Ile
 165 170 175
 Pro Thr Lys Asn Ile Glu Gly Gln Met Thr Pro Tyr Tyr Pro Val Gly
 180 185 190
 Met Gly Asn Gly Thr Pro Cys Ser Leu Lys Gln Asn Arg Pro Arg Ser
 195 200 205
 Ser Thr Val Met Tyr Ile Cys His Pro Glu Ser Lys His Glu Ile Leu
 210 215 220
 Ser Val Ala Glu Val Thr Thr Cys Glu Tyr Glu Val Val Ile Leu Thr
 225 230 235 240
 Pro Leu Leu Cys Ser His Pro Lys Tyr Arg Phe Arg Ala Ser Pro Val
 245 250 255
 Asn Asp Ile Phe Cys Gln Ser Leu Pro Gly Ser Pro Phe Lys Pro Leu
 260 265 270
 Thr Leu Arg Gln Leu Glu Gln Gln Glu Glu Ile Leu Arg Val Pro Phe
 275 280 285
 Arg Arg Asn Lys Glu Glu Asp Leu Gln Ser Thr Lys Glu Glu Arg Phe
 290 295 300
 Pro Ala Ile His Lys Ser Ile Ala Ile Gly Ser Gln Pro Val Leu Thr
 305 310 315 320
 Val Gly Thr Thr His Ile Ser Lys Leu Thr Asp Asp Gln Leu Ile Lys
 325 330 335
 Glu Phe Leu Ser Gly Ser Tyr Cys Phe Arg Gly Gly Val Gly Trp Trp
 340 345 350
 Lys Tyr Glu Phe Cys Tyr Gly Lys His Val His Gln Tyr His Glu Asp
 355 360 365
 Lys Asp Ser Gly Lys Thr Ser Val Val Val Gly Thr Trp Asn Gln Glu

59/233

370	375	380
Glu His Ile Glu Trp Ala Lys Lys Asn Thr Ala Arg Ala Tyr His Leu		
385	390	395
Gln Asp Asp Gly Thr Gln Thr Val Arg Met Val Ser His Phe Tyr Gly		400
	405	410
Asn Gly Asp Ile Cys Asp Ile Thr Asp Lys Pro Arg Gln Val Thr Val		415
	420	425
Lys Leu Lys Cys Lys Glu Ser Asp Ser Pro His Ala Val Thr Val Tyr		430
	435	440
Met Leu Glu Pro His Ser Cys Gln Tyr Ile Leu Gly Val Glu Ser Pro		445
	450	455
Val Ile Cys Lys Ile Leu Asp Thr Ala Asp Glu Asn Gly Leu Leu Ser		460
	465	470
Leu Pro Asn		475
		480

<210> 35

<211> 607

<212> PRT

<213> Homo sapiens

<400> 35

Met Gly Phe Glu Glu Leu Leu Glu Gln Val Gly Gly Phe Gly Pro Phe		
1	5	10
Gln Leu Arg Asn Val Ala Leu Leu Ala Leu Pro Arg Val Leu Leu Pro		15
	20	25
Leu His Phe Leu Leu Pro Ile Phe Leu Ala Ala Val Pro Ala His Arg		30
	35	40
Cys Ala Leu Pro Gly Ala Pro Ala Asn Phe Ser His Gln Asp Val Trp		45
	50	55
Leu Glu Ala His Leu Pro Arg Glu Pro Asp Gly Thr Leu Ser Ser Cys		60
	65	70
Leu Arg Phe Ala Tyr Pro Gln Ala Leu Pro Asn Thr Thr Leu Gly Glu		75
	80	85
Glu Arg Gln Ser Arg Gly Glu Leu Glu Asp Glu Pro Ala Thr Val Pro		90
	95	100
		105
		110

60/233

Cys Ser Gln Gly Trp Glu Tyr Asp His Ser Glu Phe Ser Ser Thr Ile
 115 120 125
 Ala Thr Glu Ser Gln Val Gly Ile Tyr Ile Ile His Leu Glu Val Glu
 130 135 140
 Cys Arg Trp Arg Gln Ser Pro Trp Glu Ala Ala Gly Arg Gly Leu Pro
 145 150 155 160
 Trp Glu Glu Ala Glu Ala Ala Gly Leu Gly Arg Asp Lys Val Ser Tyr
 165 170 175
 Ser Pro Ser Trp Arg Glu Ser Leu Gly Gly Leu Leu Ser Gly Met Glu
 180 185 190
 Trp Asp Leu Val Cys Glu Gln Lys Gly Leu Asn Arg Ala Ala Ser Thr
 195 200 205
 Phe Phe Phe Ala Gly Val Leu Val Gly Ala Val Ala Phe Gly Tyr Leu
 210 215 220
 Ser Asp Arg Phe Gly Arg Arg Arg Leu Leu Leu Val Ala Tyr Val Ser
 225 230 235 240
 Thr Leu Val Leu Gly Leu Ala Ser Ala Ala Ser Val Ser Tyr Val Met
 245 250 255
 Phe Ala Ile Thr Arg Thr Leu Thr Gly Ser Ala Leu Ala Gly Phe Thr
 260 265 270
 Ile Ile Val Met Pro Leu Glu Leu Glu Trp Leu Asp Val Glu His Arg
 275 280 285
 Thr Val Ala Gly Val Leu Ser Ser Thr Phe Trp Thr Gly Gly Val Met
 290 295 300
 Leu Leu Ala Leu Val Gly Tyr Leu Ile Arg Asp Trp Arg Trp Leu Leu
 305 310 315 320
 Leu Ala Val Thr Leu Pro Cys Ala Pro Gly Ile Leu Ser Leu Trp Trp
 325 330 335
 Val Pro Glu Ser Ala Arg Trp Leu Leu Thr Gln Gly His Val Lys Glu
 340 345 350
 Ala His Arg Tyr Leu Leu His Cys Ala Arg Leu Asn Gly Arg Pro Val
 355 360 365
 Cys Glu Asp Ser Phe Ser Gln Glu Ala Val Ser Lys Val Ala Ala Gly
 370 375 380
 Glu Arg Val Val Arg Arg Pro Ser Tyr Leu Asp Leu Phe Arg Thr Pro

61/233

385	390	395	400
Arg Leu Arg His Ile Ser Leu Cys Cys Val Val Val Trp Phe Gly Val			
405	410	415	
Asn Phe Ser Tyr Tyr Gly Leu Ser Leu Asp Val Ser Gly Leu Gly Leu			
420	425	430	
Asn Val Tyr Gln Thr Gln Leu Leu Phe Gly Ala Val Glu Leu Pro Ser			
435	440	445	
Lys Leu Leu Val Tyr Leu Ser Val Arg Tyr Ala Gly Arg Arg Leu Thr			
450	455	460	
Gln Ala Gly Thr Leu Leu Gly Thr Ala Leu Ala Phe Gly Thr Arg Leu			
465	470	475	480
Leu Val Ser Ser Asp Met Lys Ser Trp Ser Thr Val Leu Ala Val Met			
485	490	495	
Gly Lys Ala Phe Ser Glu Ala Ala Phe Thr Thr Ala Tyr Leu Phe Thr			
500	505	510	
Ser Glu Leu Tyr Pro Thr Val Leu Arg Gln Thr Gly Met Gly Leu Thr			
515	520	525	
Ala Leu Val Gly Arg Leu Gly Gly Ser Leu Ala Pro Leu Ala Ala Leu			
530	535	540	
Leu Asp Gly Val Trp Leu Ser Leu Pro Lys Leu Thr Tyr Gly Gly Ile			
545	550	555	560
Ala Leu Leu Ala Ala Gly Thr Ala Leu Leu Leu Pro Glu Thr Arg Gln			
565	570	575	
Ala Gln Leu Pro Glu Thr Ile Gln Asp Val Glu Arg Lys Ser Ala Pro			
580	585	590	
Thr Ser Leu Gln Glu Glu Glu Met Pro Met Lys Gln Val Gln Asn			
595	600	605	

<210> 36

<211> 314

<212> PRT

<213> Homo sapiens

<400> 36

Met Gly Ala Arg Gly Ala Leu Leu Leu Ala Leu Leu Leu Ala Arg Ala

1

5

10

15

62/233

Gly Leu Arg Lys Pro Glu Ser Gln Glu Ala Ala Pro Leu Ser Gly Pro
 20 25 30
 Cys Gly Arg Arg Val Ile Thr Ser Arg Ile Val Gly Gly Glu Asp Ala
 35 40 45
 Glu Leu Gly Arg Trp Pro Trp Gln Gly Ser Leu Arg Leu Trp Asp Ser
 50 55 60
 His Val Cys Gly Val Ser Leu Leu Ser His Arg Trp Ala Leu Thr Ala
 65 70 75 80
 Ala His Cys Phe Glu Thr Tyr Ser Asp Leu Ser Asp Pro Ser Gly Trp
 85 90 95
 Met Val Gln Phe Gly Gln Leu Thr Ser Met Pro Ser Phe Trp Ser Leu
 100 105 110
 Gln Ala Tyr Tyr Thr Arg Tyr Phe Val Ser Asn Ile Tyr Leu Ser Pro
 115 120 125
 Arg Tyr Leu Gly Asn Ser Pro Tyr Asp Ile Ala Leu Val Lys Leu Ser
 130 135 140
 Ala Pro Val Thr Tyr Thr Lys His Ile Gln Pro Ile Cys Leu Gln Ala
 145 150 155 160
 Ser Thr Phe Glu Phe Glu Asn Arg Thr Asp Cys Trp Val Thr Gly Trp
 165 170 175
 Gly Tyr Ile Lys Glu Asp Glu Ala Leu Pro Ser Pro His Thr Leu Gln
 180 185 190
 Glu Val Gln Val Ala Ile Ile Asn Asn Ser Met Cys Asn His Leu Phe
 195 200 205
 Leu Lys Tyr Ser Phe Arg Lys Asp Ile Phe Gly Asp Met Val Cys Ala
 210 215 220
 Gly Asn Ala Gln Gly Gly Lys Asp Ala Cys Phe Gly Asp Ser Gly Gly
 225 230 235 240
 Pro Leu Ala Cys Asn Lys Asn Gly Leu Trp Tyr Gln Ile Gly Val Val
 245 250 255
 Ser Trp Gly Val Gly Cys Gly Arg Pro Asn Arg Pro Gly Val Tyr Thr
 260 265 270
 Asn Ile Ser His His Phe Glu Trp Ile Gln Lys Leu Met Ala Gln Ser
 275 280 285
 Gly Met Ser Gln Pro Asp Pro Ser Trp Pro Leu Leu Phe Phe Pro Leu

63/233

290 295 300
 Leu Trp Ala Leu Pro Leu Leu Gly Pro Val
 305 310

 <210> 37
 <211> 94
 <212> PRT
 <213> Homo sapiens
 <400> 37
 Met Glu Leu Ser Asp Val Thr Leu Ile Glu Gly Val Gly Asn Glu Val
 1 5 10 15
 Met Val Val Ala Gly Val Val Val Leu Ile Leu Ala Leu Val Leu Ala
 20 25 30
 Trp Leu Ser Thr Tyr Val Ala Asp Ser Gly Ser Asn Gln Leu Leu Gly
 35 40 45
 Ala Ile Val Ser Ala Gly Asp Thr Ser Val Leu His Leu Gly His Val
 50 55 60
 Asp His Leu Val Ala Gly Gln Gly Asn Pro Glu Pro Thr Glu Leu Pro
 65 70 75 80
 His Pro Ser Glu Ala Asn Thr Ser Leu Asp Lys Lys Ala Arg
 85 90

<210> 38
 <211> 218
 <212> PRT
 <213> Homo sapiens
 <400> 38
 Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln Leu Ile Met
 1 5 10 15
 Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp Gly Cys Phe
 20 25 30
 Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg Arg Lys Pro
 35 40 45
 Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala Ala Val Leu
 50 55 60

64/233

Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp Phe Ala Leu
 65 70 75 80
 Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala Tyr Ile Gly
 85 90 95
 Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met Tyr Ser Arg
 100 105 110
 Thr Val Ala Ile Ile Gly Gly Leu Ser Cys Val Gly Gln Arg Cys Trp
 115 120 125
 Gly Ala Val Pro Pro Glu Thr Ser Gln Pro Leu Pro Ala Val His Arg
 130 135 140
 Pro Gly Val Pro Gly Tyr Leu Pro His Leu Cys Gly Leu Leu Thr Ala
 145 150 155 160
 Ala Gln Gln Gly Gly Pro Ala Gly Val Ser Glu Pro Ser Pro Arg Arg
 165 170 175
 Gly Ala Asp Asp Pro Ala Val Leu Arg Ala Val Trp His Pro Gly Pro
 180 185 190
 Gly Leu Ser Val Arg Leu Leu Arg Asp Pro Arg Cys Pro Asp Pro Gly
 195 200 205
 Cys Thr Ala Ala Pro Cys His Ala Ala His
 210 215

<210> 39

<211> 460

<212> PRT

<213> Homo sapiens

<400> 39

Met Phe Thr Ile Lys Leu Leu Leu Phe Ile Val Pro Leu Val Ile Ser
 1 5 10 15
 Ser Arg Ile Asp Gln Asp Asn Ser Ser Phe Asp Ser Leu Ser Pro Glu
 20 25 30
 Pro Lys Ser Arg Phe Ala Met Leu Asp Asp Val Lys Ile Leu Ala Asn
 35 40 45
 Gly Leu Leu Gln Leu Gly His Gly Leu Lys Asp Phe Val His Lys Thr
 50 55 60
 Lys Gly Gln Ile Asn Asp Ile Phe Gln Lys Leu Asn Ile Phe Asp Gln

65/233

65	70	75	80
Ser Phe Tyr Asp Leu Ser Leu Gln Thr Ser Glu Ile Lys Glu Glu Glu			
85	90	95	
Lys Glu Leu Arg Arg Thr Thr Tyr Lys Leu Gln Val Lys Asn Glu Glu			
100	105	110	
Val Lys Asn Met Ser Leu Glu Leu Asn Ser Lys Leu Glu Ser Leu Leu			
115	120	125	
Glu Glu Lys Ile Leu Leu Gln Gln Lys Val Lys Tyr Leu Glu Glu Gln			
130	135	140	
Leu Thr Asn Leu Ile Gln Asn Gln Pro Glu Thr Pro Glu His Pro Glu			
145	150	155	160
Val Thr Ser Leu Lys Thr Phe Val Glu Lys Gln Asp Asn Ser Ile Lys			
165	170	175	
Asp Leu Leu Gln Thr Val Glu Asp Gln Tyr Lys Gln Leu Asn Gln Gln			
180	185	190	
His Ser Gln Ile Lys Glu Ile Glu Asn Gln Leu Arg Arg Thr Ser Ile			
195	200	205	
Gln Glu Pro Thr Glu Ile Ser Leu Ser Ser Lys Pro Arg Ala Pro Arg			
210	215	220	
Thr Thr Pro Phe Leu Gln Leu Asn Glu Ile Arg Asn Val Lys His Asp			
225	230	235	240
Gly Ile Pro Ala Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu His Thr			
245	250	255	
Ser Gly Met Tyr Ala Ile Arg Pro Ser Asn Ser Gln Val Phe His Val			
260	265	270	
Tyr Cys Asp Val Ile Ser Gly Ser Pro Trp Thr Leu Ile Gln His Arg			
275	280	285	
Ile Asp Gly Ser Gln Asn Phe Asn Glu Thr Trp Glu Asn Tyr Lys Tyr			
290	295	300	
Gly Phe Gly Arg Leu Asp Gly Glu Phe Trp Leu Gly Leu Glu Lys Ile			
305	310	315	320
Tyr Ser Ile Val Lys Gln Ser Asn Tyr Val Leu Arg Ile Glu Leu Glu			
325	330	335	
Asp Trp Lys Asp Asn Lys His Tyr Ile Glu Tyr Ser Phe Tyr Leu Gly			
340	345	350	

66/233

Asn His Glu Thr Asn Tyr Thr Leu His Leu Val Ala Ile Thr Gly Asn
 355 360 365
 Val Pro Asn Ala Ile Pro Glu Asn Lys Asp Leu Val Phe Ser Thr Trp
 370 375 380
 Asp His Lys Ala Lys Gly His Phe Asn Cys Pro Glu Gly Tyr Ser Gly
 385 390 395 400
 Gly Trp Trp Trp His Asp Glu Cys Gly Glu Asn Asn Leu Asn Gly Lys
 405 410 415
 Tyr Asn Lys Pro Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg Gly Leu
 420 425 430
 Ser Trp Lys Ser Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser Thr Lys
 435 440 445
 Met Leu Ile His Pro Thr Asp Ser Glu Ser Phe Glu
 450 455 460

<210> 40

<211> 216

<212> PRT

<213> Homo sapiens

<400> 40

Met Val Pro Met His Leu Leu Gly Arg Leu Glu Lys Pro Leu Leu Leu
 1 5 10 15
 Leu Cys Cys Ala Ser Phe Leu Leu Gly Leu Ala Leu Leu Gly Ile Lys
 20 25 30
 Thr Asp Ile Thr Pro Val Ala Tyr Phe Phe Leu Thr Leu Gly Gly Phe
 35 40 45
 Phe Leu Phe Ala Tyr Leu Leu Val Arg Phe Leu Glu Trp Gly Leu Arg
 50 55 60
 Ser Gln Leu Gln Ser Met Gln Thr Glu Ser Pro Gly Pro Ser Gly Asn
 65 70 75 80
 Ala Arg Asp Asn Glu Ala Phe Glu Val Pro Val Tyr Glu Glu Ala Val
 85 90 95
 Val Gly Leu Glu Ser Gln Cys Arg Pro Gln Glu Leu Asp Gln Pro Pro
 100 105 110
 Pro Tyr Ser Thr Val Val Ile Pro Pro Ala Pro Glu Glu Glu Gln Pro

67/233

115	120	125
Ser His Pro Glu Gly Ser Arg Arg Ala Lys Leu Glu Gln Arg Arg Met		
130	135	140
Ala Ser Glu Gly Ser Met Ala Gln Glu Gly Ser Pro Gly Arg Ala Pro		
145	150	155
Ile Asn Leu Arg Leu Arg Gly Pro Arg Ala Val Ser Thr Ala Pro Asp		
165	170	175
Leu Gln Ser Leu Ala Ala Val Pro Thr Leu Glu Pro Leu Thr Pro Pro		
180	185	190
Pro Ala Tyr Asp Val Cys Phe Gly His Pro Asp Asp Asp Ser Val Phe		
195	200	205
Tyr Glu Asp Asn Trp Ala Pro Pro		
210	215	

<210> 41

<211> 4335

<212> DNA

<213> Homo sapiens

<400> 41

atgcagggcc caccgctcct gaccgcccgc cacctcctct gcgtgtgcac cgccgcgctg	60
gccgtggctc ccgggcctcg gtttctggtg acagccccag ggatcatcag gcccgaggga	120
aatgtgacta ttgggggtgga gcttctggaa cactgcccctt cacaggtgac tgtgaaggcg	180
gagctgctca agacagcacc aaacctcact gtctctgtcc tggaagcaga aggagtcttt	240
gaaaaaggct cttttaagac acttactctt ccatcactac ctctgaacag tgcagatgag	300
atztatgagc tacgtgtaac cggacgtacc caggatgaga ttttattctc taatagtacc	360
cgttatcat ttgagaccaa gagaatatct gtcttcattc aaacagacaa ggccttatac	420
aagccaaagc aagaagtga gtttcgcatt gttacactct tctcagattt taagccttac	480
aaaacctctt taaacattct cattaaggac cccaaatcaa atttgatcca acagtgggtg	540
tcacaacaaa gtgatcttgg agtcatttcc aaaacttttc agctatcttc ccatccaata	600
cttggtgact ggtctattca agttcaagtg aatgaccaga catattatca atcatttcag	660
gtttcagaat atgtattacc aaaatttgaa gtgactttgc agacaccatt atattgttct	720
atgaattcta agcattttaa tggtagcacc acggcaaagt atacatatgg gaagccagtg	780
aaaggagacg taacgcttac atttttacct ttatcctttt ggggaaagaa gaaaaatatt	840
acaaaaacat ttaagataaa tggatctgca aacttctctt ttaatgatga agagatgaaa	900
aatgtaatgg attcttcaaa tggactttct gaatacctgg atctatcttt ccttggaaca	960

68/233

gtagaaat	ttt	taaccacagt	gacagaatca	gttacaggta	tttcaagaaa	tgtaagcact	1020	
aatgtgttct	tcaagcaaca	tgattacatc	attgagtttt	ttgattatac	tactgtcttg		1080	
aagccatctc	tcaacttcac	agccactgtg	aaggtaactc	gtgctgatgg	caaccaactg		1140	
actcttgaag	aaagaagaaa	taatgtagtc	ataacagtga	cacagagaaa	ctatactgag		1200	
tactggagcg	gatctaacag	tggaaatcag	aaaatggaag	ctgttcagaa	aataaattat		1260	
actgtccccc	aaagtggaac	ttttaagatt	gaattcccaa	tcctggagga	ttccagttag		1320	
ctacagttga	aggcctat	ttt	ccttggtagt	aaaagtagca	tggcagttca	tagtctgttt	1380	
aagtctccta	gtaagacata	catccaacta	aaaacaagag	atgaaaatat	aaaggtggga		1440	
tgcctttttg	agttggtggt	tagtggaac	aaacgattga	aggagttaag	ctatatggta		1500	
gtatccaggg	gacagttggt	ggctgtagga	aaacaaaatt	caacaatgtt	ctctttaaca		1560	
ccagaaaatt	cttggaactc	aaaagcctgt	gtaattgtgt	attatattga	agatgatggg		1620	
gaaattataa	gtgatgttct	aaaaattcct	gttcagcttg	tttttaaaaa	taagataaag		1680	
ctatatggga	gtaaagtga	agctgaacca	tctgagaaag	tctctcttag	gatctctgtg		1740	
acacagcctg	actccatagt	tgggattgta	gctgttgaca	aaagtgtgaa	tctgatgaat		1800	
gcctctaatt	atattacaat	ggaaaatgtg	gtccatgagt	tggaaactta	taacacagga		1860	
tattatttag	gcatgttcat	gaattctttt	gcagtctttc	aggaatgtgg	actctgggta		1920	
ttgacagatg	caaaccctac	gaaggattat	attgatgggtg	tttatgacaa	tgacagaatat		1980	
gctgagaggt	ttatggagga	aaatgaagga	catattgtag	atattcatga	cttttctttg		2040	
ggtagcagtc	cacatgtcog	aaagcatttt	ccagagactt	ggatttggtc	agacaccaac		2100	
atgggttcca	ggatttacca	agaatttgaa	gtaactgtac	ctgattctat	cacttcttgg		2160	
gtggctactg	gttttgtgat	ctctgaggac	ctgggtcttg	gactaacaac	tactccagtg		2220	
gagctccaag	ccttccaacc	atttttcatt	tttttgaatc	ttccctactc	tgttatcaga		2280	
ggtgaagaat	ttgctttgga	aataactata	ttcaattatt	tgaagatgc	cactgagggt		2340	
aaggtaatca	ttgagaaaag	tgacaaat	gatattctaa	tgacttcaag	tgaataaat		2400	
gccacaggcc	accagcagac	ccttctggtt	cccagttagg	atggggcaac	tgttcttttt		2460	
cccatcaggc	caacacatct	gggagaaatt	cctatcacag	tcacagctct	ttcaccact		2520	
gcttctgatg	ctatcaccca	gatgatttta	gtaaaggctg	aaggaataga	aaaatcatat		2580	
tcacaatcca	tcttattaga	cttgactgac	aataggctac	agagtaccct	gaaaactttg		2640	
agtttctcat	ttcctcctaa	tacagtgact	ggcagtga	gagttcagat	cactgcaatt		2700	
ggagatgttc	ttggtccttc	catcaatggc	ttagcctcat	tgattcggat	gccttatggc		2760	
tgtggtgaac	agaacatgat	aaat	ttt	gct	ccaaaatattt	acattttgga	ttatctgact	2820
aaaaagaaac	aactgacaga	taatttgaaa	gaaaaagctc	tttcatttat	gaggcaaggt		2880	
taccagagag	aacttctcta	tcagagggaa	gatggctctt	tcagtgcctt	tgggaattat		2940	
gaccctctg	ggagcacttg	gttgctcagct	tttgttttaa	gatgtttcct	tgaagccgat		3000	
ccttacatag	atattgatca	gaatgtgtta	cacagaacat	acacttggtc	taaaggacat		3060	

69/233

cagaaatcca acggtgaatt ttgggatcca ggaagagtga ttcatagtga gcttcaaggt 3120
 ggcaataaaa gtccagtaac acttacagcc tatattgtaa cttctctcct gggatataga 3180
 aagtatcagc ctaacattga tgtgcaagag totatccatt ttttggagtc tgaattcagt 3240
 agaggaattt cagacaatta tactotagcc cttataactt atgcattgtc atcagtggg 3300
 agtcctaaag cgaaggaagc tttgaatatg ctgacttggg gagcagaaca agaaggtggc 3360
 atgcaattct ggggtgcatc agagtccaaa ctttctgact cctggcagcc acgctccctg 3420
 gatattgaag ttgcagccta tgcactgctc tcacacttct tacaatttca gacttctgag 3480
 ggaatcccaa ttatgaggtg gctaagcagg caaagaaata gcttgggtgg ttttgcactc 3540
 actcaggata ccactgtggc tttaaaggct ctgtctgaat ttgcagccct aatgaataca 3600
 gaaaggacaa atatccaagt gaccgtgacg gggcctagct caccaagtc tgtaaagttt 3660
 ctgattgaca cacacaaccg cttactcctt cagacagcag agcttgctgt ggtacagcca 3720
 acggcagtta atatttccgc aaatggtttt ggatttgcta tttgtcagct caatgttgta 3780
 tataatgtga aggcttctgg gtcttctaga agacgaagat ctatccaaaa tcaagaagcc 3840
 tttgatttag atgttgctgt aaaagaaaat aaagatgac tcaatcatgt ggatttgaat 3900
 gtgtgtacaa gcttttcggg ccgggtagg agtggcatgg ctcttatgga agttaacct 3960
 ttaagtggct ttatgggtgc ttcagaagca atttctctga gcgagacagt gaagaaagt 4020
 gaatatgatc atggaaaact caacctctat ttagattctg taaatgaaac ccagttttgt 4080
 gttaatatct ctgctgtgag aaactttaaa gtttcaaata cccaagatgc ttcagtgtcc 4140
 atagtggatt actatgagcc aaggagacag gcgggtgagaa gttacaactc tgaagtgaag 4200
 ctgtcctcct gtgacctttg cagtgatgtc cagggctgcc gtccttgtga ggatggagct 4260
 tcaggctccc atcatcactc ttcagtcatt tttattttct gtttcaagct tctgtacttt 4320
 atggaacttt ggctg 4335

<210> 42

<211> 1746

<212> DNA

<213> Homo sapiens

<400> 42

atgttccccg cgggcccccc cagccacagc ctccctccggc tccccctgct gcagttgctg 60
 ctactgggtg tgcaggccgt ggggaggggg ctgggcccgc ccagccccgc cgggggcccc 120
 ctggaagatg tggtcacga gaggtaccac atccccagg cctgtccccg ggaagtgcag 180
 atgggggatt ttgtgcgcta ccactacaac ggcacttttg aagatggcaa gaagtttgat 240
 tcaagctatg atcgcaacac cttgggtggc atcgtgggtg gtgtggggcg cctcatcact 300
 ggcatggacc gaggcctcat gggcatgtgt gtcaacgagc ggcgacgcct catttgtcct 360
 cccacactgg gctatgggag catcggcctg gcggggctca ttccaccgga tgccaccctc 420

70/233

tacttcgatg tggttctgct ggatgtgtgg aacaaggaag acaccgtgca ggtgagcaca 480
 ttgctgcgcc cgccccactg ccccgcatg gtccaggacg gcgactttgt ccgctaccac 540
 tacaatggca ccctgctgga cggcacctcc ttccacacca gctacagtaa gggcggcact 600
 tatgacacct acgtcggctc tggttggctg atcaagggca tggaccaggg gctgctgggc 660
 atgtgtcctg gagagagaag gaagattatc atccctccat tcctggccta tggcgagaaa 720
 ggctatggga cggatgaccc cccacaggcc tcgctggtct ttcacgtcct cctgattgac 780
 gtgcacaacc cgaaggacgc tgtccagcta gagacgctgg agctcccccc cggtgtgtgc 840
 cgcagagccg gggccgggga ctccatgcgc taccactaca atggctcctt gatggacggc 900
 accctcttcg attccagcta ctcccgcaac cacacctaca atacctatat cgggcagggt 960
 tacatcatcc ccgggatgga ccaggggctg caggggtgcct gcatggggga acgccggaga 1020
 attaccatcc ccccgccact cgccatgagg gagaatggaa ctggagacaa gatccctggc 1080
 tctgcctgc taatcttcaa cgtccatgtc attgacttcc acaaccctgc ggatgtggtg 1140
 gaaatcagga cactgtcccg gccatctgag acctgcaatg agaccaccaa gcttggggac 1200
 tttgttcgat accattacaa ctgttctttg ctggacggca ccagctgtt cacctcgcct 1260
 gactacgggg cccccagga ggcgactctc ggggcccaaca aggtgatcga aggcctggac 1320
 acgggcctgc agggcatgtg tgtgggagag agggcgagc tcactgtgcc ccgcacctg 1380
 gccacgggg agagtggagc ccggggagtc ccaggcagtg ctgtgctgct gtttgagggtg 1440
 gagctggtgt ccggggagga tgggctgccc acaggctacc tgtttgtgtg gcacaaggac 1500
 cctcctgcca acctgtttga agacatggac ctcaacaagg atggcgaggc cctccggag 1560
 gagttctcca ccttcatcaa ggctcaagtg agtgagggca aaggacgcct catgcctggg 1620
 caggaccctg agaaaaccat aggagacatg ttccagaacc aggaccgcaa ccaggacggc 1680
 aagatcacag tcgacgagct caagctgaag tcagatgagg acgaggagcg ggtccacgag 1740
 gagctc 1746

<210> 43

<211> 1230

<212> DNA

<213> Homo sapiens

<400> 43

atggagcttc cctcagggcc ggggccggag cggtcttttg actcgacccg gcttcgggt 60
 gactgcttcc tactgctcgt gctgctgctc tacgcgccag tcgggttctg cctcctcgtc 120
 ctgcgcctct ttctcgggat ccacgtcttc ctggtcagct gcgcgctgcc agacagcgtc 180
 cttcgcagat tcgtagtgcg gaccatgtgt gcggtgctag ggctcgtggc ccggcaggag 240
 gactccggac tccgggatca cagtgtcagg gtcctcattt ccaacctatg gacaccttc 300
 gaccacaaca tagtcaattt gcttaccacc tgtagcacc ctctactcaa tagtcccccc 360

71/233

```

agctttgtgt gctggtctcg gggcttcatg gagatgaatg ggcgggggga gttggtggag 420
tcaactcaaga gattctgtgc ttccacgagg cttcccccca ctctctgct getattccct 480
gaggaagagg ccaccaatgg cggggagggg ctctgcgct toagttcctg gccattttct 540
atccaagatg tggtaacaacc tcttaccctg caagttcaga gacctctggt ctctgtgacg 600
gtgtcagatg cctcctgggt ctccagaactg ctgtggtcac ttttcgtccc ttccacgggtg 660
tatcaagtaa ggtggtctcg tctgttcat cgccaactag ggggaagcgaa tgaggagttt 720
gcactccgtg tacaacagct ggtggccaag gaattgggcc agacagggac acggtcact 780
ccagctgaca aagcagagca catgaagcga caaagacacc ccagattgcg cccccagtca 840
gccagtcctt ctttccctcc ctcccctggt ccttctcctg atgtgcaact ggcaactctg 900
gtcagagag tcaaggaagt tttgccccat gtgccattgg gtgtcatcca gagagacctg 960
gccaaactg gctgtgtaga cttgactatc actaatctgc ttgagggggc cgtagctttc 1020
atgcctgaag acatcaccaa gggaaactcag tccctaccca cagcctctgc ctccaagttt 1080
cccagctctg gcccggtgac cctcagcca acagccctaa catttgccaa gtcttcctgg 1140
gcccggcagg agagcctgca ggagcgcaag caagcactat atgaatacgc aagaaggaga 1200
ttcacagaga gacgagccca ggaggtgac 1230

```

<210> 44

<211> 1449

<212> DNA

<213> Homo sapiens

<400> 44

```

atggaggaag gaggcggcgg cgtacggagt ctggtcccg ggcggccggt gttactggtc 60
ctctgcggcc tcttgaggc gtccggcggc ggcgagccc ttctcaact cagcgatgac 120
atccctttcc gagtcaactg gcccggcacc gagtctctc tgcacacaa tggagtttta 180
tataaagaag ataattatgt catcatgaca actgcacata aagaaaaata taaatgcata 240
cttccccttg tgacaagtgg ggatgaggaa gaagaaaagg attataaagg ccctaattcca 300
agagagcttt tggagccact atttaacaa agcagttgtt cctacagaat tgagtcttat 360
tggacttacg aagtatgtca tggaaaacac attcggcagt accatgaaga gaaagaaact 420
ggtcagaaaa taaatattca cgagtactac cttgggaata tgttgccaa gaaccttcta 480
tttgaaaaag aacgagaagc agaagaaaag gaaaaatcaa atgagattcc cactaaaaat 540
atcgaaggtc agatgacacc atactatcct gtgggaatgg gaaatggtac acctttagt 600
ttgaaacaga accggcccag atcaagtaact gtgatgtaca tatgtcatcc tgaatctaag 660
catgaaattc tttcagtagc tgaagttaca acttgtgaat atgaagttgt cattttgaca 720
ccactcttgt gcagtcaccc taaatatagg ttcagagcat ctctgtgaa tgacatattt 780
tgtcaatcac tgccaggatc tccatttaag cccctcacc tgaggcagct ggagcagcag 840

```

72/233

gaagaaatac taaggggtgcc ttttaggaga aataaagagg aagatttgca atcaactaaa	900
gaagagagat ttccagcgat ccacaagtcg attgctattg gctctcagcc agtgctcact	960
gttgggacaa cccacatato caaattgaca gatgaccaac tcataaaaga gtttcttagt	1020
ggttcttact gctttcgtgg ggggtgtcggg tgggtggaaat atgaattctg ctatggcaaa	1080
catgtacatc aataccatga ggacaaggat agtgggaaaa cctctgtggg tgtcgggaca	1140
tggaaccaag aagagcatat tgaatgggct aagaagaata ctgctagagc ttatcatctt	1200
caagacgatg gtacccagac agtcaggatg gtgtcacatt tttatggaaa tggagatatt	1260
tgtgatataa ctgacaaacc aagacaggtg actgtaaaac taaagtgcaa agaatcagat	1320
tcacctcatg ctgttactgt atatatgcta gagcctcact cctgtcaata tattcttggg	1380
gttgaatctc cagtgatctg taaaatctta gatacagcag atgaaaatgg acttctttct	1440
ctccccaac	1449

<210> 45

<211> 1821

<212> DNA

<213> Homo sapiens

<400> 45

atgggctttg aggagctgct ggagcaggtg ggcggctttg ggcccttcca actgcggaat	60
gtggcactgc tggccctgcc ccgagtgtgt ctaccactgc acttctctct gcccatcttc	120
ctggctgccg tgccctgcca ccgatgtgcc ctgccgggtg cccctgccaa cttcagccat	180
caggatgtgt ggctggaggc ccactctccc cgggagcctg atggcacgct cagctcctgc	240
ctccgctttg cctatcccca ggctctcccc aacaccacgt tgggggaaga aaggcagagc	300
cgtggggagc tggaggatga acctgccaca gtgccctgct ctccaggctg ggagtaagac	360
cactcagaat tctcctctac cattgcaact gagtcccagg tcggtattta cataatccat	420
ctggagggtg aatgtcgggt gaggcagttc ccctgggagg cagcaggctg aggccttct	480
tgggaagaag ctgaggctgc aggactgggg agggacaaag tttctattc cccaagctgg	540
cgtgaatcgt tgggaggttt attatctggc atggagtggg atctggtgtg tgagcagaaa	600
ggtctgaaca gagctgcgtc cactttcttc ttcccggtg tgctggtggg ggctgtggcc	660
tttgatatac tgtccgacag gtttgggcgg cggcgtctgc tgctggtagc ctacgtgagt	720
acctggtgc tgggcctggc atctgcagcc tccgtcagct atgtaatgtt tgccatcacc	780
cgcacctta ctggctcagc cctggctggg tttaccatca tcgtgatgcc actggagctg	840
gagtggctgg atgtggagca ccgcaccgtg gctggagtcc tgagcagcac cttctggaca	900
gggggcgtga tgctgtggc actgggtggg tacctgatac gggactggcg atggcttctg	960
ctagctgtca ccctgccttg tgcccaggc atcctcagcc tctggtgggt gctgagttct	1020
gcacgctggc ttctgaccca aggccatgtg aaagaggccc acaggtaact gctccactgt	1080

73/233

```

gccaggetca atgggcggcc agtgtgtgag gacagettca gccaggaggc tgtgagcaaa 1140
gtggccgccc gggaacgggt ggtccgaaga ccttcatacc tagacctgtt ccgcacacca 1200
cggctccgac acatctcact gtgctgcgtg gtggtgtggt tcggagtga cttctcctat 1260
tacggcctga gtctggatgt gtcggggctg gggctgaacg tgtaccagac acagctgttg 1320
ttcggggctg tggaactgcc ctccaagctg ctggtctact tgcggtgcg ctacgcagga 1380
cgccgcctca cgcaagccgg gacactgctg ggcacggccc tggcgttcgg cactagactg 1440
ctagtgtcct ctgatatgaa gtccctggagc actgtccctgg cagtgatggg gaaagctttt 1500
tctgaagctg ccttcaccac tgcctacctg ttcacttcag agttgtaccc taagggtgctc 1560
agacagacag ggatggggct gactgcaactg gtgggcgggc tggggggctc tttggcccca 1620
ctggcgccct tgcctggatgg agtgtggctg tcaactgccc agcttactta tggggggatc 1680
gccctgctgg ctgccggcac cgccctcctg ctgccagaga cgaggcaggc acagctgcc 1740
gagaccatcc aggacgtgga gagaaagagt gcccacaacca gtcttcagga ggaagagatg 1800
cccatgaagc aggtccagaa c 1821

```

<210> 46

<211> 942

<212> DNA

<213> Homo sapiens

<400> 46

```

atgggcgcgc gcggggcgct gctgctggcg ctgctgctgg ctcggtctgg actcaggaag 60
ccggagtgcg aggaggcggc gccgttatca ggaccatgcg gccgacgggt catcacgtcg 120
cgcatcgtgg gtggagagga cgccgaactc gggcggttggc cgtggcaggg gagcctgcgc 180
ctgtgggatt cccacgtatg cggagtgage ctgctcagcc accgctgggc actcacggcg 240
gcgcaactgt ttgaaacctc tagtgacctt agtgatccct ccgggtggat ggtccagttt 300
ggccagctga cttccatgcc atccttctgg agcctgcagg cctactacac ccgttacttc 360
gtatcgaata tctatctgag ccctcgctac ctggggaatt caccctatga cattgccttg 420
gtgaagctgt ctgcacctgt cacctacact aaacacatcc agcccatctg tctccaggcc 480
tccacatttg agtttgagaa ccggacagac tgctgggtga ctggctgggg gtacatcaaa 540
gaggatgagg cactgccatc tccccacacc ctccaggaag ttcaggctgc catcataaac 600
aactctatgt gcaaccacct ctctctcaag tacagtttcc gcaaggacat ctttgagac 660
atggtttgtg ctggcaatgc ccaaggcggg aaggatgcct gcttcggtga ctcagggtga 720
cccttgccct gtaacaagaa tggactgtgg tatcagattg gactcgtgag ctggggagtg 780
ggctgtggtc ggcccaatcg gcccggtgtc tacaccaata tcagccacca ctttgagtgg 840
atccagaagc tgatggccca gactggcatg tccagccag accctcctg gcgctactc 900
ttttccctc ttctctgggc tctccactc ctggggcgcg tc 942

```

74/233

<210> 47

<211> 282

<212> DNA

<213> Homo sapiens

<400> 47

atggagctct	ctgatgtcac	cctcattgag	ggtgtgggta	atgaggtgat	ggtggtggca	60
ggtgtggtgg	tgtgtattct	agccttggtc	ctagcttggc	tctctacct	cgtagcagac	120
agcggtagca	accagctcct	gggcgtatt	gtgtcagcag	gcgacacatc	cgctctccac	180
ctggggcatg	tggaccacct	ggtggcaggc	caaggcaacc	ccgagccaac	tgaactcccc	240
catccatcag	aggcaaatac	ttccctggac	aagaaagcca	ga		282

<210> 48

<211> 654

<212> DNA

<213> Homo sapiens

<400> 48

atggcgtcga	agatagggtc	gagacggtgg	atgttgacgc	tgatcatgca	gttgggttcg	60
gtgtgtctca	cacgtgccc	cttttggggc	tgtttcagcc	agctcatgct	gtacgctgag	120
agggctgagg	cacgccggaa	gcccgacatc	ccagtgcctt	acctgtattt	cgacatgggg	180
gcagccgtgc	tgtgcgctag	tttcatgtcc	tttggcgtag	agcggcgctg	gttcgcgctg	240
ggggccgcac	tccaattggc	cattagcacc	tacgcgcctt	acatcggggg	ctacgtccac	300
tacggggact	ggtgaaggt	ccgtatgtac	tgcgcacag	ttgccatcat	cggcgggactt	360
tcttgtgttg	gccagcggtg	ctggggagct	gtaccgccgg	aaacctcgca	gccgtccctt	420
gcagtccacc	ggccagggtg	tcctgggtat	ctacctatc	tgtgtggcct	actcactgca	480
gcacagcaag	gaggaccggc	tggcgtatct	gaaccatctc	ccaggagggg	agctgatgat	540
ccagctgttc	ttcgtgctgt	atggcatcct	ggccctggcc	tttctgtcag	gtactacgt	600
gacctcgtct	gccagatcc	tggctgtact	gtgccccct	gtcatgctgc	tcct	654

<210> 49

<211> 1380

<212> DNA

<213> Homo sapiens

<400> 49

atgttcacaa	ttaagctcct	tctttttatt	gttctctag	ttatttctc	cagaattgat	60
------------	------------	------------	-----------	-----------	------------	----

75/233

caagacaatt catcatttga ttctctatct ccagagccaa aatcaagatt tgctatgtta	120
gacgatgtaa aaatttttagc caatggcctc cttcagttgg gacatggtct taaagacttt	180
gtccataaga cgaagggccca aattaatgac atattttcaaa aactcaacat atttgatcag	240
tctttttatg atctatcgct gcaaaccagt gaaatcaaaag aagaagaaaa ggaactgaga	300
agaactacat ataaactaca agtcaaaaat gaagaggtaa agaatatgtc acttgaactc	360
aactcaaaac ttgaaagcct cctagaagaa aaaattctac ttcaacaaaa agtgaaatat	420
ttagaagagc aactaactaa cttaattcaa aatcaacctg aaactccaga acaccagaa	480
gtaaacttcac ttaaaacttt tgtagaaaaa caagataata gcatcaaga ccttctccag	540
accgtggaag accaatataa acaattaaac caacagcata gtcaaataaa agaaatagaa	600
aatcagctca gaaggactag tattcaagaa cccacagaaa tttctctatc ttccaagcca	660
agagcaccaa gaactactcc ctttcttcag ttgaatgaaa taagaaatgt aaaacatgat	720
ggcattcctg ctgaatgtac caccatttat aacagagggtg aacatacaag tggcatgtat	780
gccatcagac ccagcaactc tcaagttttt catgtctact gtgatgttat atcaggtagt	840
ccatggacat taattcaaca tcgaatagat ggatcacaaa acttcaatga aacgtgggag	900
aactacaaat atggttttggt gaggcttgat ggagaatttt ggttgggcct agagaagata	960
tactccatag tgaagcaatc taattatgtt ttacgaattg agctggaaga ctggaaagac	1020
aacaaacatt atattgaata ttctttttac ttgggaaatc acgaaaccaa ctatacgcta	1080
catctagttg cgattactgg caatgtcccc aatgcaatcc cggaaaacaa agatttggtg	1140
ttttctactt gggatcacaa agcaaaaagga cacttcaact gtccagagggt ttattcagga	1200
ggctggtggt ggcattgatga gtgtggagaa aacaacctaa atggtaaata taacaaacca	1260
agagcaaaat ctaagccaga gaggagaaga ggattatctt ggaagtctca aaatggaagg	1320
ttatactcta taaaatcaac caaatgttg atccatccaa cagattcaga aagctttgaa	1380

<210> 50

<211> 648

<212> DNA

<213> Homo sapiens

<400> 50

atggtgccaa tgcacttact ggggagactg gagaagccgc ttctcctcct gtgctgcgcc	60
tccttcctac tggggctggc tttgctgggc ataaagacgg acatcacccc ogttgcttat	120
ttctttctca cattgggtgg cttctttcttg tttgectatc tcctgggtccg gtttctggaa	180
tgggggcttc ggtcccagct ccaatcaatg cagactgaga gccaggggcc ctcaggcaat	240
gcacgggaca atgaagcctt tgaagtgcc gtctatgaag aggccgtggt gggactagaa	300
tccagtgcc gcccccaga gttggacca ccacccccct acagcactgt tgtgataccc	360
ccagcacctg aggaggaaca acctagccat ccagaggggt ccaggagagc caaactggaa	420

76/233

cagaggcgaa tggcctcaga ggggtccatg gcccaggaag gaagccctgg aagagctcca 480
 atcaaccttc ggcttcgggg accacgggct gtgtccactg ctctgatct gcagagcttg 540
 gcggcagtcc ccacattaga gcctctgact ccaccccctg cctatgatgt ctgctttggt 600
 caccctgatg atgatagtgt tttttatgag gacaactggg caccacct 648

<210> 51

<211> 4473

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (45)...(4382)

<400> 51

aacttccccg gcagcggact gtagcccagg cagacgccgt cgag atg cag ggc cca 56

Met Gln Gly Pro

1

ccg ctc ctg acc gcc gcc cac ctc ctc tgc gtg tgc acc gcc gcg ctg 104

Pro Leu Leu Thr Ala Ala His Leu Leu Cys Val Cys Thr Ala Ala Leu

5

10

15

20

gcc gtg gct ccc ggg cct cgg ttt ctg gtg aca gcc cca ggg atc atc 152

Ala Val Ala Pro Gly Pro Arg Phe Leu Val Thr Ala Pro Gly Ile Ile

25

30

35

agg ccc gga gga aat gtg act att ggg gtg gag ctt ctg gaa cac tgc 200

Arg Pro Gly Gly Asn Val Thr Ile Gly Val Glu Leu Leu Glu His Cys

40

45

50

cct tca cag gtg act gtg aag gcg gag ctg ctc aag aca gca tca aac 248

Pro Ser Gln Val Thr Val Lys Ala Glu Leu Leu Lys Thr Ala Ser Asn

55

60

65

ctc act gtc tct gtc ctg gaa gca gaa gga gtc ttt gaa aaa ggc tct 296

Leu Thr Val Ser Val Leu Glu Ala Glu Gly Val Phe Glu Lys Gly Ser

70

75

80

ttt aag aca ctt act ctt cca tca cta cct ctg aac agt gca gat gag 344

Phe Lys Thr Leu Thr Leu Pro Ser Leu Pro Leu Asn Ser Ala Asp Glu

85

90

95

100

att tat gag cta cgt gta acc gga cgt acc cag gat gag att tta ttc 392

77/233

Ile Tyr Glu Leu Arg Val Thr Gly Arg Thr Gln Asp Glu Ile Leu Phe	
105	110 115
tct aat agt acc cgc tta tca ttt gag acc aag aga ata tct gtc ttc	440
Ser Asn Ser Thr Arg Leu Ser Phe Glu Thr Lys Arg Ile Ser Val Phe	
120	125 130
att caa aca gac aag gcc tta tac aag cca aag caa gaa gtg aag ttt	488
Ile Gln Thr Asp Lys Ala Leu Tyr Lys Pro Lys Gln Glu Val Lys Phe	
135	140 145
cgc att gtt aca ctc ttc tca gat ttt aag cct tac aaa acc tct tta	536
Arg Ile Val Thr Leu Phe Ser Asp Phe Lys Pro Tyr Lys Thr Ser Leu	
150	155 160
aac att ctc att aag gac ccc aaa tca aat ttg atc caa cag tgg ttg	584
Asn Ile Leu Ile Lys Asp Pro Lys Ser Asn Leu Ile Gln Gln Trp Leu	
165	170 175 180
tca caa caa agt gat ctt gga gtc att tcc aaa act ttt cag cta tct	632
Ser Gln Gln Ser Asp Leu Gly Val Ile Ser Lys Thr Phe Gln Leu Ser	
185	190 195
tcc cat cca ata ctt ggt gac tgg tct att caa gtt caa gtg aat gac	680
Ser His Pro Ile Leu Gly Asp Trp Ser Ile Gln Val Gln Val Asn Asp	
200	205 210
cag aca tat tat caa tca ttt cag gtt tca gaa tat gta tta cca aaa	728
Gln Thr Tyr Tyr Gln Ser Phe Gln Val Ser Glu Tyr Val Leu Pro Lys	
215	220 225
ttt gaa gtg act ttg cag aca cca tta tat tgt tct atg aat tct aag	776
Phe Glu Val Thr Leu Gln Thr Pro Leu Tyr Cys Ser Met Asn Ser Lys	
230	235 240
cat tta aat ggt acc atc acg gca aag tat aca tat ggg aag cca gtg	824
His Leu Asn Gly Thr Ile Thr Ala Lys Tyr Thr Tyr Gly Lys Pro Val	
245	250 255 260
aaa gga gac gta acg ctt aca ttt tta cct tta tcc ttt tgg gga aag	872
Lys Gly Asp Val Thr Leu Thr Phe Leu Pro Leu Ser Phe Trp Gly Lys	
265	270 275
aag aaa aat att aca aaa aca ttt aag ata aat gga tct gca aac ttc	920
Lys Lys Asn Ile Thr Lys Thr Phe Lys Ile Asn Gly Ser Ala Asn Phe	
280	285 290

78/233

tct ttt aat gat gaa gag atg aaa aat gta atg gat tct tca aat gga	968
Ser Phe Asn Asp Glu Glu Met Lys Asn Val Met Asp Ser Ser Asn Gly	
295 300 305	
ctt tct gaa tac ctg gat cta tct ttc cct gga cca gta gaa att tta	1016
Leu Ser Glu Tyr Leu Asp Leu Ser Phe Pro Gly Pro Val Glu Ile Leu	
310 315 320	
acc aca gtg aca gaa tca gtt aca ggt att tca aga aat gta agc act	1064
Thr Thr Val Thr Glu Ser Val Thr Gly Ile Ser Arg Asn Val Ser Thr	
325 330 335 340	
aat gtg ttc ttc aag caa cat gat tac atc att gag ttt ttt gat tat	1112
Asn Val Phe Phe Lys Gln His Asp Tyr Ile Ile Glu Phe Phe Asp Tyr	
345 350 355	
act act gtc ttg aag cca tct ctc aac ttc aca gcc act gtg aag gta	1160
Thr Thr Val Leu Lys Pro Ser Leu Asn Phe Thr Ala Thr Val Lys Val	
360 365 370	
act cgt gct gat ggc aac caa ctg act ctt gaa gaa aga aga aat aat	1208
Thr Arg Ala Asp Gly Asn Gln Leu Thr Leu Glu Glu Arg Arg Asn Asn	
375 380 385	
gta gtc ata aca gtg aca cag aga aac tat act gag tac tgg agc gga	1256
Val Val Ile Thr Val Thr Gln Arg Asn Tyr Thr Glu Tyr Trp Ser Gly	
390 395 400	
tct aac agt gga aat cag aaa atg gaa gct gtt cag aaa ata aat tat	1304
Ser Asn Ser Gly Asn Gln Lys Met Glu Ala Val Gln Lys Ile Asn Tyr	
405 410 415 420	
act gtc ccc caa agt gga act ttt aag att gaa ttc cca atc ctg gag	1352
Thr Val Pro Gln Ser Gly Thr Phe Lys Ile Glu Phe Pro Ile Leu Glu	
425 430 435	
gat tcc agt gag cta cag ttg aag gcc tat ttc ctt ggt agt aaa agt	1400
Asp Ser Ser Glu Leu Gln Leu Lys Ala Tyr Phe Leu Gly Ser Lys Ser	
440 445 450	
agc atg gca gtt cat agt ctg ttt aag tct cct agt aag aca tac atc	1448
Ser Met Ala Val His Ser Leu Phe Lys Ser Pro Ser Lys Thr Tyr Ile	
455 460 465	
caa cta aaa aca aga gat gaa aat ata aag gtg gga tgg cct ttt gag	1496
Gln Leu Lys Thr Arg Asp Glu Asn Ile Lys Val Gly Ser Pro Phe Glu	

79/233

470	475	480	
ttg gtg gtt agt ggc aac aaa cga ttg aag gag tta agc tat atg gta			1544
Leu Val Val Ser Gly Asn Lys Arg Leu Lys Glu Leu Ser Tyr Met Val			
485	490	495	500
gta tcc agg gga cag ttg gtg gct gta gga aaa caa aat tca aca atg			1592
Val Ser Arg Gly Gln Leu Val Ala Val Gly Lys Gln Asn Ser Thr Met			
505	510	515	
ttc tct tta aca cca gaa aat tct tgg act cca aaa gcc tgt gta att			1640
Phe Ser Leu Thr Pro Glu Asn Ser Trp Thr Pro Lys Ala Cys Val Ile			
520	525	530	
gtg tat tat att gaa gat gat ggg gaa att ata agt gat gtt cta aaa			1688
Val Tyr Tyr Ile Glu Asp Asp Gly Glu Ile Ile Ser Asp Val Leu Lys			
535	540	545	
att cct gtt cag ctt gtt ttt aaa aat aag ata aag cta tat tgg agt			1736
Ile Pro Val Gln Leu Val Phe Lys Asn Lys Ile Lys Leu Tyr Trp Ser			
550	555	560	
aaa gtg aaa gct gaa cca tct gag aaa gtc tct ctt agg atc tct gtg			1784
Lys Val Lys Ala Glu Pro Ser Glu Lys Val Ser Leu Arg Ile Ser Val			
565	570	575	580
aca cag cct gac tcc ata gtt ggg att gta gct gtt gac aaa agt gtg			1832
Thr Gln Pro Asp Ser Ile Val Gly Ile Val Ala Val Asp Lys Ser Val			
585	590	595	
aat ctg atg aat gcc tct aat gat att aca atg gaa aat gtg gtc cat			1880
Asn Leu Met Asn Ala Ser Asn Asp Ile Thr Met Glu Asn Val Val His			
600	605	610	
gag ttg gaa ctt tat aac aca gga tat tat tta ggc atg ttc atg aat			1928
Glu Leu Glu Leu Tyr Asn Thr Gly Tyr Tyr Leu Gly Met Phe Met Asn			
615	620	625	
tct ttt gca gtc ttt cag gaa tgt gga ctc tgg gta ttg aca gat gca			1976
Ser Phe Ala Val Phe Gln Glu Cys Gly Leu Trp Val Leu Thr Asp Ala			
630	635	640	
aac ctc acg aag gat tat att gat ggt gtt tat gac aat gca gaa tat			2024
Asn Leu Thr Lys Asp Tyr Ile Asp Gly Val Tyr Asp Asn Ala Glu Tyr			
645	650	655	660
gct gag agg ttt atg gag gaa aat gaa gga cat att gta gat att cat			2072

80/233

Ala Glu Arg Phe Met Glu Glu Asn Glu Gly His Ile Val Asp Ile His	
665 670 675	
gac ttt tct ttg ggt agc agt cca cat gtc cga aag cat ttt cca gag	2120
Asp Phe Ser Leu Gly Ser Ser Pro His Val Arg Lys His Phe Pro Glu	
680 685 690	
act tgg att tgg cta gac acc aac atg ggt tcc agg att tac caa gaa	2168
Thr Trp Ile Trp Leu Asp Thr Asn Met Gly Ser Arg Ile Tyr Gln Glu	
695 700 705	
ttt gaa gta act gta cct gat tct atc act tct tgg gtg gct act ggt	2216
Phe Glu Val Thr Val Pro Asp Ser Ile Thr Ser Trp Val Ala Thr Gly	
710 715 720	
ttt gtg atc tct gag gac ctg ggt ctt gga cta aca act act cca gtg	2264
Phe Val Ile Ser Glu Asp Leu Gly Leu Gly Leu Thr Thr Thr Pro Val	
725 730 735 740	
gag ctc caa gcc ttc caa cca ttt ttc att ttt ttg aat ctt ccc tac	2312
Glu Leu Gln Ala Phe Gln Pro Phe Phe Ile Phe Leu Asn Leu Pro Tyr	
745 750 755	
tct gtt atc aga ggt gaa gaa ttt gct ttg gaa ata act ata ttc aat	2360
Ser Val Ile Arg Gly Glu Glu Phe Ala Leu Glu Ile Thr Ile Phe Asn	
760 765 770	
tat ttg aaa gat gcc act gag gtt aag gta atc att gag aaa agt gac	2408
Tyr Leu Lys Asp Ala Thr Glu Val Lys Val Ile Ile Glu Lys Ser Asp	
775 780 785	
aaa ttt gat att cta atg act tca agt gaa ata aat gcc aca ggc cac	2456
Lys Phe Asp Ile Leu Met Thr Ser Ser Glu Ile Asn Ala Thr Gly His	
790 795 800	
cag cag acc ctt ctg gtt ccc agt gag gat ggg gca act gtt ctt ttt	2504
Gln Gln Thr Leu Leu Val Pro Ser Glu Asp Gly Ala Thr Val Leu Phe	
805 810 815 820	
ccc atc agg cca aca cat ctg gga gaa att cct atc aca gtc aca gct	2552
Pro Ile Arg Pro Thr His Leu Gly Glu Ile Pro Ile Thr Val Thr Ala	
825 830 835	
ctt tca ccc act gct tct gat gct atc acc cag atg att tta gta aag	2600
Leu Ser Pro Thr Ala Ser Asp Ala Ile Thr Gln Met Ile Leu Val Lys	
840 845 850	

81/233

gct gaa gga ata gaa aaa tca tat tca caa tcc atc tta tta gac ttg	2648
Ala Glu Gly Ile Glu Lys Ser Tyr Ser Gln Ser Ile Leu Leu Asp Leu	
855 860 865	
act gac aat agg cta cag agt acc ctg aaa act ttg agt ttc tca ttt	2696
Thr Asp Asn Arg Leu Gln Ser Thr Leu Lys Thr Leu Ser Phe Ser Phe	
870 875 880	
cct cct aat aca gtg act ggc agt gaa aga gtt cag atc act gca att	2744
Pro Pro Asn Thr Val Thr Gly Ser Glu Arg Val Gln Ile Thr Ala Ile	
885 890 895 900	
gga gat gtt ctt ggt cct tcc atc aat ggc tta gcc tca ttg att cgg	2792
Gly Asp Val Leu Gly Pro Ser Ile Asn Gly Leu Ala Ser Leu Ile Arg	
905 910 915	
atg cct tat ggc tgt ggt gaa cag aac atg ata aat ttt gct cca aat	2840
Met Pro Tyr Gly Cys Gly Glu Gln Asn Met Ile Asn Phe Ala Pro Asn	
920 925 930	
att tac att ttg gat tat ctg act aaa aag aaa caa ctg aca gat aat	2888
Ile Tyr Ile Leu Asp Tyr Leu Thr Lys Lys Lys Gln Leu Thr Asp Asn	
935 940 945	
ttg aaa gaa aaa gct ctt tca ttt atg agg caa ggt tac cag aga gaa	2936
Leu Lys Glu Lys Ala Leu Ser Phe Met Arg Gln Gly Tyr Gln Arg Glu	
950 955 960	
ctt ctc tat cag agg gaa gat ggc tct ttc agt gct ttt ggg aat tat	2984
Leu Leu Tyr Gln Arg Glu Asp Gly Ser Phe Ser Ala Phe Gly Asn Tyr	
965 970 975 980	
gac cct tct ggg agc act tgg ttg tca gct ttt gtt tta aga tgt ttc	3032
Asp Pro Ser Gly Ser Thr Trp Leu Ser Ala Phe Val Leu Arg Cys Phe	
985 990 995	
ctt gaa gcc gat cct tac ata gat att gat cag aat gtg tta cac aga	3080
Leu Glu Ala Asp Pro Tyr Ile Asp Ile Asp Gln Asn Val Leu His Arg	
1000 1005 1010	
aca tac act tgg ctt aaa gga cat cag aaa tcc aac ggt gaa ttt tgg	3128
Thr Tyr Thr Trp Leu Lys Gly His Gln Lys Ser Asn Gly Glu Phe Trp	
1015 1020 1025	
gat cca gga aga gtg att cat agt gag ctt caa ggt ggc aat aaa agt	3176
Asp Pro Gly Arg Val Ile His Ser Glu Leu Gln Gly Gly Asn Lys Ser	

82/233

1030	1035	1040	
cca gta aca ctt aca gcc tat att gta act tct ctc ctg gga tat aga			3224
Pro Val Thr Leu Thr Ala Tyr Ile Val Thr Ser Leu Leu Gly Tyr Arg			
1045	1050	1055	1060
aag tat cag cct aac att gat gtg caa gag tct atc cat ttt ttg gag			3272
Lys Tyr Gln Pro Asn Ile Asp Val Gln Glu Ser Ile His Phe Leu Glu			
1065	1070	1075	
tct gaa ttc agt aga gga att tca gac aat tat act cta gcc ctt ata			3320
Ser Glu Phe Ser Arg Gly Ile Ser Asp Asn Tyr Thr Leu Ala Leu Ile			
1080	1085	1090	
act tat gca ttg tca tca gtg ggg agt cct aaa gcg aag gaa gct ttg			3368
Thr Tyr Ala Leu Ser Ser Val Gly Ser Pro Lys Ala Lys Glu Ala Leu			
1095	1100	1105	
aat atg ctg act tgg aga gca gaa caa gaa ggt ggc atg caa ttc tgg			3416
Asn Met Leu Thr Trp Arg Ala Glu Gln Glu Gly Gly Met Gln Phe Trp			
1110	1115	1120	
gtg tca tca gag tcc aaa ctt tct gac tcc tgg cag cca cgc tcc ctg			3464
Val Ser Ser Glu Ser Lys Leu Ser Asp Ser Trp Gln Pro Arg Ser Leu			
1125	1130	1135	1140
gat att gaa gtt gca gcc tat gca ctg ctc tca cac ttc tta caa ttt			3512
Asp Ile Glu Val Ala Ala Tyr Ala Leu Leu Ser His Phe Leu Gln Phe			
1145	1150	1155	
cag act tct gag gga atc cca att atg agg tgg cta agc agg caa aga			3560
Gln Thr Ser Glu Gly Ile Pro Ile Met Arg Trp Leu Ser Arg Gln Arg			
1160	1165	1170	
aat agc ttg ggt ggt ttt gca tct act cag gat acc act gtg gct tta			3608
Asn Ser Leu Gly Gly Phe Ala Ser Thr Gln Asp Thr Thr Val Ala Leu			
1175	1180	1185	
aag gct ctg tct gaa ttt gca gcc cta atg aat aca gaa agg aca aat			3656
Lys Ala Leu Ser Glu Phe Ala Ala Leu Met Asn Thr Glu Arg Thr Asn			
1190	1195	1200	
atc caa gtg acc gtg acg ggg cct agc tca cca agt cct gta aag ttt			3704
Ile Gln Val Thr Val Thr Gly Pro Ser Ser Pro Ser Pro Val Lys Phe			
1205	1210	1215	1220
ctg att gac aca cac aac cgc tta ctc ctt cag aca gca gag ctt gct			3752

83/233

Leu Ile Asp Thr His Asn Arg Leu Leu Leu Gln Thr Ala Glu Leu Ala	
1225 1230 1235	
gtg gta cag cca acg gca gtt aat att tcc gca aat ggt ttt gga ttt	3800
Val Val Gln Pro Thr Ala Val Asn Ile Ser Ala Asn Gly Phe Gly Phe	
1240 1245 1250	
gct att tgt cag ctc aat gtt gta tat aat gtg aag gct tct ggg tct	3848
Ala Ile Cys Gln Leu Asn Val Val Tyr Asn Val Lys Ala Ser Gly Ser	
1255 1260 1265	
tct aga aga cga aga tct atc caa aat caa gaa gcc ttt gat tta gat	3896
Ser Arg Arg Arg Arg Ser Ile Gln Asn Gln Glu Ala Phe Asp Leu Asp	
1270 1275 1280	
gtt gct gta aaa gaa aat aaa gat gat ctc aat cat gtg gat ttg aat	3944
Val Ala Val Lys Glu Asn Lys Asp Asp Leu Asn His Val Asp Leu Asn	
1285 1290 1295 1300	
gtg tgt aca agc ttt tcg ggc ccg ggt agg agt ggc atg gct ctt atg	3992
Val Cys Thr Ser Phe Ser Gly Pro Gly Arg Ser Gly Met Ala Leu Met	
1305 1310 1315	
gaa gtt aac cta tta agt ggc ttt atg gtg cct tca gaa gca att tct	4040
Glu Val Asn Leu Leu Ser Gly Phe Met Val Pro Ser Glu Ala Ile Ser	
1320 1325 1330	
ctg agc gag aca gtg aag aaa gtg gaa tat gat cat gga aaa ctc aac	4088
Leu Ser Glu Thr Val Lys Lys Val Glu Tyr Asp His Gly Lys Leu Asn	
1335 1340 1345	
ctc tat tta gat tct gta aat gaa acc cag ttt tgt gtt aat att cct	4136
Leu Tyr Leu Asp Ser Val Asn Glu Thr Gln Phe Cys Val Asn Ile Pro	
1350 1355 1360	
gct gtg aga aac ttt aaa gtt tca aat acc caa gat gct tca gtg tcc	4184
Ala Val Arg Asn Phe Lys Val Ser Asn Thr Gln Asp Ala Ser Val Ser	
1365 1370 1375 1380	
ata gtg gat tac tat gag cca agg aga cag gcg gtg aga agt tac aac	4232
Ile Val Asp Tyr Tyr Glu Pro Arg Arg Gln Ala Val Arg Ser Tyr Asn	
1385 1390 1395	
tct gaa gtg aag ctg tcc tcc tgt gac ctt tgc agt gat gtc cag ggc	4280
Ser Glu Val Lys Leu Ser Ser Cys Asp Leu Cys Ser Asp Val Gln Gly	
1400 1405 1410	

84/233

tgc cgt cct tgt gag gat gga gct tca ggc tcc cat cat cac tct tca 4328
 Cys Arg Pro Cys Glu Asp Gly Ala Ser Gly Ser His His His Ser Ser
 1415 1420 1425
 gtc att ttt att ttc tgt ttc aag ctt ctg tac ttt atg gaa ctt tgg 4376
 Val Ile Phe Ile Phe Cys Phe Lys Leu Leu Tyr Phe Met Glu Leu Trp
 1430 1435 1440
 ctg tgatttattt ttaaaggact ctgtgtaaca ctaacatttc cagtagtcac a 4430
 Leu
 1445
 tgtgattgtt ttgttttcgt agaagaatac tgcttctatt ttg 4473

<210> 52

<211> 2630

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (82)...(1830)

<400> 52

agttctggga ggcgggggga aggaggttgg tggcgactcc ctcgctcgcc ctcaactgccg 60
 gcggtcccaa ctccaggcac c atg ttc ccc gcg ggc ccc ccc agc cac agc 111
 Met Phe Pro Ala Gly Pro Pro Ser His Ser
 1 5 10
 ctc ctc cgg ctc ccc ctg ctg cag ttg ctg cta ctg gtg gtg cag gcc 159
 Leu Leu Arg Leu Pro Leu Leu Gln Leu Leu Leu Val Val Gln Ala
 15 20 25
 gtg ggg agg ggg ctg ggc cgc gcc agc ccg gcc ggg ggc ccc ctg gaa 207
 Val Gly Arg Gly Leu Gly Arg Ala Ser Pro Ala Gly Gly Pro Leu Glu
 30 35 40
 gat gtg gtc atc gag agg tac cac atc ccc agg gcc tgt ccc cgg gaa 255
 Asp Val Val Ile Glu Arg Tyr His Ile Pro Arg Ala Cys Pro Arg Glu
 45 50 55
 gtg cag atg ggg gat ttt gtg cgc tac cac tac aac ggc act ttt gaa 303
 Val Gln Met Gly Asp Phe Val Arg Tyr His Tyr Asn Gly Thr Phe Glu
 60 65 70

85/233

gat ggc aag aag ttt gat tca agc tat gat cgc aac acc ttg gtg gcc	351
Asp Gly Lys Lys Phe Asp Ser Ser Tyr Asp Arg Asn Thr Leu Val Ala	
75 80 85 90	
atc gtg gtg ggt gtg ggg cgc ctc atc act ggc atg gac cga ggc ctc	399
Ile Val Val Gly Val Gly Arg Leu Ile Thr Gly Met Asp Arg Gly Leu	
95 100 105	
atg ggc atg tgt gtc aac gag cgg cga cgc ctc att gtg cct ccc cac	447
Met Gly Met Cys Val Asn Glu Arg Arg Arg Leu Ile Val Pro Pro His	
110 115 120	
ctg ggc tat ggg agc atc ggc ctg gcg ggg ctc att cca ccg gat gcc	495
Leu Gly Tyr Gly Ser Ile Gly Leu Ala Gly Leu Ile Pro Pro Asp Ala	
125 130 135	
acc ctc tac ttc gat gtg gtt ctg ctg gat gtg tgg aac aag gaa gac	543
Thr Leu Tyr Phe Asp Val Val Leu Leu Asp Val Trp Asn Lys Glu Asp	
140 145 150	
acc gtg cag gtg agc aca ttg ctg cgc ccg ccc cac tgc ccc cgc atg	591
Thr Val Gln Val Ser Thr Leu Leu Arg Pro Pro His Cys Pro Arg Met	
155 160 165 170	
gtc cag gac ggc gac ttt gtc cgc tac cac tac aat ggc acc ctg ctg	639
Val Gln Asp Gly Asp Phe Val Arg Tyr His Tyr Asn Gly Thr Leu Leu	
175 180 185	
gac ggc acc tcc ttc gac acc agc tac agt aag ggc ggc act tat gac	687
Asp Gly Thr Ser Phe Asp Thr Ser Tyr Ser Lys Gly Gly Thr Tyr Asp	
190 195 200	
acc tac gtc ggc tct ggt tgg ctg atc aag ggc atg gac cag ggg ctg	735
Thr Tyr Val Gly Ser Gly Trp Leu Ile Lys Gly Met Asp Gln Gly Leu	
205 210 215	
ctg ggc atg tgt cct gga gag aga agg aag att atc atc cct cca ttc	783
Leu Gly Met Cys Pro Gly Glu Arg Arg Lys Ile Ile Ile Pro Pro Phe	
220 225 230	
ctg gcc tat ggc gag aaa ggc tat ggg acg gtg atc ccc cca cag gcc	831
Leu Ala Tyr Gly Glu Lys Gly Tyr Gly Thr Val Ile Pro Pro Gln Ala	
235 240 245 250	
tcg ctg gtc ttt cac gtc ctc ctg att gac gtg cac aac ccg aag gac	879
Ser Leu Val Phe His Val Leu Leu Ile Asp Val His Asn Pro Lys Asp	

86/233

255	260	265	
gct gtc cag cta gag acg ctg gag ctc ccc ccc ggc tgt gtc cgc aga			927
Ala Val Gln Leu Glu Thr Leu Glu Leu Pro Pro Gly Cys Val Arg Arg			
270	275	280	
gcc ggg gcc ggg gac ttc atg cgc tac cac tac aat ggc tcc ttg atg			975
Ala Gly Ala Gly Asp Phe Met Arg Tyr His Tyr Asn Gly Ser Leu Met			
285	290	295	
gac ggc acc ctc ttc gat tcc agc tac tcc cgc aac cac acc tac aat			1023
Asp Gly Thr Leu Phe Asp Ser Ser Tyr Ser Arg Asn His Thr Tyr Asn			
300	305	310	
acc tat atc ggg cag ggt tac atc atc ccc ggg atg gac cag ggg ctg			1071
Thr Tyr Ile Gly Gln Gly Tyr Ile Ile Pro Gly Met Asp Gln Gly Leu			
315	320	325	330
cag ggt gcc tgc atg ggg gaa cgc cgg aga att acc atc ccc ccg cac			1119
Gln Gly Ala Cys Met Gly Glu Arg Arg Arg Ile Thr Ile Pro Pro His			
335	340	345	
ctc gcc tat ggg gag aat gga act gga gac aag atc cct ggc tct gcc			1167
Leu Ala Tyr Gly Glu Asn Gly Thr Gly Asp Lys Ile Pro Gly Ser Ala			
350	355	360	
gtg cta atc ttc aac gtc cat gtc att gac ttc cac aac cct gcg gat			1215
Val Leu Ile Phe Asn Val His Val Ile Asp Phe His Asn Pro Ala Asp			
365	370	375	
gtg gtg gaa atc agg aca ctg tcc cgg cca tct gag acc tgc aat gag			1263
Val Val Glu Ile Arg Thr Leu Ser Arg Pro Ser Glu Thr Cys Asn Glu			
380	385	390	
acc acc aag ctt ggg gac ttt gtt cga tac cat tac aac tgt tct ttg			1311
Thr Thr Lys Leu Gly Asp Phe Val Arg Tyr His Tyr Asn Cys Ser Leu			
395	400	405	410
ctg gac ggc acc cag ctg ttc acc tcg cat gac tac ggg gcc ccc cag			1359
Leu Asp Gly Thr Gln Leu Phe Thr Ser His Asp Tyr Gly Ala Pro Gln			
415	420	425	
gag gcg act ctc ggg gcc aac aag gtg atc gaa ggc ctg gac acg ggc			1407
Glu Ala Thr Leu Gly Ala Asn Lys Val Ile Glu Gly Leu Asp Thr Gly			
430	435	440	
ctg cag ggc atg tgt gtg gga gag agg cgg cag ctc atc gtg ccc ccg			1455

87/233

Leu Gln Gly Met Cys Val Gly Glu Arg Arg Gln Leu Ile Val Pro Pro

445

450

455

cac ctg gcc cac ggg gag agt gga gcc cgg gga gtc cca ggc agt gct 1503

His Leu Ala His Gly Glu Ser Gly Ala Arg Gly Val Pro Gly Ser Ala

460

465

470

gtg ctg ctg ttt gag gtg gag ctg gtg tcc cgg gag gat ggg ctg ccc 1551

Val Leu Leu Phe Glu Val Glu Leu Val Ser Arg Glu Asp Gly Leu Pro

475

480

485

490

aca ggc tac ctg ttt gtg tgg cac aag gac cct cct gcc aac ctg ttt 1599

Thr Gly Tyr Leu Phe Val Trp His Lys Asp Pro Pro Ala Asn Leu Phe

495

500

505

gaa gac atg gac ctc aac aag gat ggc gag gtc cct ccg gag gag ttc 1647

Glu Asp Met Asp Leu Asn Lys Asp Gly Glu Val Pro Pro Glu Glu Phe

510

515

520

tcc acc ttc atc aag gct caa gtg agt gag ggc aaa gga cgc ctc atg 1695

Ser Thr Phe Ile Lys Ala Gln Val Ser Glu Gly Lys Gly Arg Leu Met

525

530

535

cct ggg cag gac cct gag aaa acc ata gga gac atg ttc cag aac cag 1743

Pro Gly Gln Asp Pro Glu Lys Thr Ile Gly Asp Met Phe Gln Asn Gln

540

545

550

gac cgc aac cag gac ggc aag atc aca gtc gac gag ctc aag ctg aag 1791

Asp Arg Asn Gln Asp Gly Lys Ile Thr Val Asp Glu Leu Lys Leu Lys

555

560

565

570

tca gat gag gac gag gag cgg gtc cac gag gag ctc tga ggggcaggga 1840

Ser Asp Glu Asp Glu Glu Arg Val His Glu Glu Leu

575

580

gcctggccag gcctgagaca cagaggccca ctgcgagggg gacagtggcg gtgggactga 1900

cctgctgaca gtcaccctcc ctctgctggg atgaggtcca ggagccaact aaaacaatgg 1960

cagaggagac atctctggtg ttcccaccac cctagatgaa aatccacagc acagacctct 2020

accgtgttcc tcttccatcc ctaaaccact tccctaaaat gtttggtattt gcaaagccaa 2080

tttggggcct gtggagcctg ggggttgata gggccatggc tgggtcccca ccatacctcc 2140

cctccacatc actgacacag ctgagcttgt tatccatctc cccaaacttt ctctttcttt 2200

gtactttctg tcatccccac tcccagcccc tattctcteta tgtgacagct ggctaggacc 2260

cctctgcctt cctccccaat cctgactggc tcttagggaa ggggaaggct cctggagggc 2320

agccctacct ctcccatgcc ctttgccctc ctccctcgcc tccagtggag gctgagctga 2380

88/233

ccctgggctg ctggaggcca gactgggctg tagttagctt ttcaccccta aagaaggctt 2440
 tccctaagga accatagaag agaggaagaa aacaaagggc atgtgtgagg gaagctgctt 2500
 ggggtgggtgt tagggctatg aaatcttgga tttggggctg aggggtggga gggagggcag 2560
 agctctgcac actcaaaggc taaactgggtg tcagtccttt tttcctttgt tccaaataaa 2620
 agattaaacc 2630

<210> 53

<211> 1472

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (89)...(1321)

<400> 53

aaaaagactc cgccttccca agagcccctg cggccggggcg cgaaaatggc ggccggggcg 60
 acggccgggc gctcctgaag cagcagtt atg gag ctt ccc tca ggg ccg ggg 112

Met Glu Leu Pro Ser Gly Pro Gly

1

5

ccg gag cgg ctc ttt gac tcg cac cgg ctt ccg ggt gac tgc ttc cta 160
 Pro Glu Arg Leu Phe Asp Ser His Arg Leu Pro Gly Asp Cys Phe Leu

10

15

20

ctg ctc gtg ctg ctg ctc tac gcg cca gtc ggg ttc tgc ctc ctc gtc 208
 Leu Leu Val Leu Leu Leu Tyr Ala Pro Val Gly Phe Cys Leu Leu Val

25

30

35

40

ctg cgc ctc ttt ctc ggg atc cac gtc ttc ctg gtc agc tgc gcg ctg 256
 Leu Arg Leu Phe Leu Gly Ile His Val Phe Leu Val Ser Cys Ala Leu

45

50

55

cca gac agc gtc ctt cgc aga ttc gta gtg cgg acc atg tgt gcg gtg 304
 Pro Asp Ser Val Leu Arg Arg Phe Val Val Arg Thr Met Cys Ala Val

60

65

70

cta ggg ctc gtg gcc cgg cag gag gac tcc gga ctc cgg gat cac agt 352
 Leu Gly Leu Val Ala Arg Gln Glu Asp Ser Gly Leu Arg Asp His Ser

75

80

85

gtc agg gtc ctc att tcc aac cat gtg aca cct ttc gac cac aac ata 400
 Val Arg Val Leu Ile Ser Asn His Val Thr Pro Phe Asp His Asn Ile

89/233

90	95	100	
gtc aat ttg ctt acc acc tgt agc acc cct cta ctc aat agt ccc ccc			448
Val Asn Leu Leu Thr Thr Cys Ser Thr Pro Leu Leu Asn Ser Pro Pro			
105	110	115	120
agc ttt gtg tgc tgg tct cgg ggc ttc atg gag atg aat ggg cgg ggg			496
Ser Phe Val Cys Trp Ser Arg Gly Phe Met Glu Met Asn Gly Arg Gly			
125	130	135	
gag ttg gtg gag tca ctc aag aga ttc tgt gct tcc acg agg ctt ccc			544
Glu Leu Val Glu Ser Leu Lys Arg Phe Cys Ala Ser Thr Arg Leu Pro			
140	145	150	
ccc act cct ctg ctg cta ttc cct gag gaa gag gcc acc aat ggc cgg			592
Pro Thr Pro Leu Leu Leu Phe Pro Glu Glu Glu Ala Thr Asn Gly Arg			
155	160	165	
gag ggg ctc ctg cgc ttc agt tcc tgg cca ttt tct atc caa gat gtg			640
Glu Gly Leu Leu Arg Phe Ser Ser Trp Pro Phe Ser Ile Gln Asp Val			
170	175	180	
gta caa cct ctt acc ctg caa gtt cag aga ccc ctg gtc tct gtg acg			688
Val Gln Pro Leu Thr Leu Gln Val Gln Arg Pro Leu Val Ser Val Thr			
185	190	195	200
gtg tca gat gcc tcc tgg gtc tca gaa ctg ctg tgg tca ctt ttc gtc			736
Val Ser Asp Ala Ser Trp Val Ser Glu Leu Leu Trp Ser Leu Phe Val			
205	210	215	
cct ttc acg gtg tat caa gta agg tgg ctt cgt cct gtt cat cgc caa			784
Pro Phe Thr Val Tyr Gln Val Arg Trp Leu Arg Pro Val His Arg Gln			
220	225	230	
cta ggg gaa gcg aat gag gag ttt gca ctc cgt gta caa cag ctg gtg			832
Leu Gly Glu Ala Asn Glu Glu Phe Ala Leu Arg Val Gln Gln Leu Val			
235	240	245	
gcc aag gaa ttg ggc cag aca ggg aca cgg ctc act cca gct gac aaa			880
Ala Lys Glu Leu Gly Gln Thr Gly Thr Arg Leu Thr Pro Ala Asp Lys			
250	255	260	
gca gag cac atg aag cga caa aga cac ccc aga ttg cgc ccc cag tca			928
Ala Glu His Met Lys Arg Gln Arg His Pro Arg Leu Arg Pro Gln Ser			
265	270	275	280
gcc cag tct tct ttc cct ccc tcc cct ggt cct tct cct gat gtg caa			976

90/233

Ala Gln Ser Ser Phe Pro Pro Ser Pro Gly Pro Ser Pro Asp Val Gln
 285 290 295
 ctg gca act ctg gct cag aga gtc aag gaa gtt ttg ccc cat gtg cca 1024
 Leu Ala Thr Leu Ala Gln Arg Val Lys Glu Val Leu Pro His Val Pro
 300 305 310
 ttg ggt gtc atc cag aga gac ctg gcc aag act ggc tgt gta gac ttg 1072
 Leu Gly Val Ile Gln Arg Asp Leu Ala Lys Thr Gly Cys Val Asp Leu
 315 320 325
 act atc act aat ctg ctt gag ggg gcc gta gct ttc atg cct gaa gac 1120
 Thr Ile Thr Asn Leu Leu Glu Gly Ala Val Ala Phe Met Pro Glu Asp
 330 335 340
 atc acc aag gga act cag tcc cta ccc aca gcc tct gcc tcc aag ttt 1168
 Ile Thr Lys Gly Thr Gln Ser Leu Pro Thr Ala Ser Ala Ser Lys Phe
 345 350 355 360
 ccc agc tct ggc ccg gtg acc cct cag cca aca gcc cta aca ttt gcc 1216
 Pro Ser Ser Gly Pro Val Thr Pro Gln Pro Thr Ala Leu Thr Phe Ala
 365 370 375
 aag tct tcc tgg gcc cgg cag gag agc ctg cag gag cgc aag caa gca 1264
 Lys Ser Ser Trp Ala Arg Gln Glu Ser Leu Gln Glu Arg Lys Gln Ala
 380 385 390
 cta tat gaa tac gca aga agg aga ttc aca gag aga cga gcc cag gag 1312
 Leu Tyr Glu Tyr Ala Arg Arg Arg Phe Thr Glu Arg Arg Ala Gln Glu
 395 400 405
 gct gac tgagctcaaa ggaacaggat ggcacccaga gccgcaggac ggagactggg gg 1370
 Ala Asp
 410
 cagccctcac ccaactcaca acaggctgga tgggtgggtg gtaaaaaggg aaggatgagg 1430
 ctcccccaat gtcacattaa attcatggtt ttcattcaag gc 1472

<210> 54

<211> 1652

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

91/233

<222> (17)...(1468)

<400> 54

```

aaagcggcgg cggagg atg gag gaa gga ggc ggc ggc gta cgg agt ctg gtc      52
      Met Glu Glu Gly Gly Gly Gly Val Arg Ser Leu Val
              1              5              10

ccg ggc ggg ccg gtg tta ctg gtc ctc tgc ggc ctc ctg gag gcg tcc      100
Pro Gly Gly Pro Val Leu Leu Val Leu Cys Gly Leu Leu Glu Ala Ser
      15              20              25

ggc ggc ggc cga gcc ctt cct caa ctc agc gat gac atc cct ttc cga      148
Gly Gly Gly Arg Ala Leu Pro Gln Leu Ser Asp Asp Ile Pro Phe Arg
      30              35              40

gtc aac tgg ccc ggc acc gag ttc tct ctg ccc aca act gga gtt tta      196
Val Asn Trp Pro Gly Thr Glu Phe Ser Leu Pro Thr Thr Gly Val Leu
      45              50              55              60

tat aaa gaa gat aat tat gtc atc atg aca act gca cat aaa gaa aaa      244
Tyr Lys Glu Asp Asn Tyr Val Ile Met Thr Thr Ala His Lys Glu Lys
      65              70              75

tat aaa tgc ata ctt ccc ctt gtg aca agt ggg gat gag gaa gaa gaa      292
Tyr Lys Cys Ile Leu Pro Leu Val Thr Ser Gly Asp Glu Glu Glu Glu
      80              85              90

aag gat tat aaa ggc cct aat cca aga gag ctt ttg gag cca cta ttt      340
Lys Asp Tyr Lys Gly Pro Asn Pro Arg Glu Leu Leu Glu Pro Leu Phe
      95              100              105

aaa caa agc agt tgt tcc tac aga att gag tct tat tgg act tac gaa      388
Lys Gln Ser Ser Cys Ser Tyr Arg Ile Glu Ser Tyr Trp Thr Tyr Glu
      110              115              120

gta tgt cat gga aaa cac att cgg cag tac cat gaa gag aaa gaa act      436
Val Cys His Gly Lys His Ile Arg Gln Tyr His Glu Glu Lys Glu Thr
      125              130              135              140

ggt cag aaa ata aat att cac gag tac tac ctt ggg aat atg ttg gcc      484
Gly Gln Lys Ile Asn Ile His Glu Tyr Tyr Leu Gly Asn Met Leu Ala
      145              150              155

aag aac ctt cta ttt gaa aaa gaa cga gaa gca gaa gaa aag gaa aaa      532
Lys Asn Leu Leu Phe Glu Lys Glu Arg Glu Ala Glu Glu Lys Glu Lys
      160              165              170

```

92/233

tca aat gag att ccc act aaa aat atc gaa ggt cag atg aca cca tac	580
Ser Asn Glu Ile Pro Thr Lys Asn Ile Glu Gly Gln Met Thr Pro Tyr	
175 180 185	
tat cct gtg gga atg gga aat ggt aca cct tgt agt ttg aaa cag aac	628
Tyr Pro Val Gly Met Gly Asn Gly Thr Pro Cys Ser Leu Lys Gln Asn	
190 195 200	
cgg ccc aga tca agt act gtg atg tac ata tgt cat cct gaa tct aag	676
Arg Pro Arg Ser Ser Thr Val Met Tyr Ile Cys His Pro Glu Ser Lys	
205 210 215 220	
cat gaa att ctt tca gta gct gaa gtt aca act tgt gaa tat gaa gtt	724
His Glu Ile Leu Ser Val Ala Glu Val Thr Thr Cys Glu Tyr Glu Val	
225 230 235	
gtc att ttg aca cca ctc ttg tgc agt cat cct aaa tat agg ttc aga	772
Val Ile Leu Thr Pro Leu Leu Cys Ser His Pro Lys Tyr Arg Phe Arg	
240 245 250	
gca tct cct gtg aat gac ata ttt tgt caa tca ctg cca gga tct cca	820
Ala Ser Pro Val Asn Asp Ile Phe Cys Gln Ser Leu Pro Gly Ser Pro	
255 260 265	
ttt aag ccc ctc acc ctg agg cag ctg gag cag cag gaa gaa ata cta	868
Phe Lys Pro Leu Thr Leu Arg Gln Leu Glu Gln Gln Glu Glu Ile Leu	
270 275 280	
agg gtg cct ttt agg aga aat aaa gag gaa gat ttg caa tca act aaa	916
Arg Val Pro Phe Arg Arg Asn Lys Glu Glu Asp Leu Gln Ser Thr Lys	
285 290 295 300	
gaa gag aga ttt cca gcg atc cac aag tcg att gct att ggc tct cag	964
Glu Glu Arg Phe Pro Ala Ile His Lys Ser Ile Ala Ile Gly Ser Gln	
305 310 315	
cca gtg ctc act gtt ggg aca acc cac ata tcc aaa ttg aca gat gac	1012
Pro Val Leu Thr Val Gly Thr Thr His Ile Ser Lys Leu Thr Asp Asp	
320 325 330	
caa ctc ata aaa gag ttt ctt agt ggt tct tac tgc ttt cgt ggg ggt	1060
Gln Leu Ile Lys Glu Phe Leu Ser Gly Ser Tyr Cys Phe Arg Gly Gly	
335 340 345	
gtc ggt tgg tgg aaa tat gaa ttc tgc tat ggc aaa cat gta cat caa	1108
Val Gly Trp Trp Lys Tyr Glu Phe Cys Tyr Gly Lys His Val His Gln	

93/233

350	355	360	
tac cat gag gac aag gat agt ggg aaa acc tct gtg gtt gtc ggg aca			1156
Tyr His Glu Asp Lys Asp Ser Gly Lys Thr Ser Val Val Val Gly Thr			
365	370	375	380
tgg aac caa gaa gag cat att gaa tgg gct aag aag aat act gct aga			1204
Trp Asn Gln Glu Glu His Ile Glu Trp Ala Lys Lys Asn Thr Ala Arg			
385	390	395	
gct tat cat ctt caa gac gat ggt acc cag aca gtc agg atg gtg tca			1252
Ala Tyr His Leu Gln Asp Asp Gly Thr Gln Thr Val Arg Met Val Ser			
400	405	410	
cat ttt tat gga aat gga gat att tgt gat ata act gac aaa cca aga			1300
His Phe Tyr Gly Asn Gly Asp Ile Cys Asp Ile Thr Asp Lys Pro Arg			
415	420	425	
cag gtg act gta aaa cta aag tgc aaa gaa tca gat tca cct cat gct			1348
Gln Val Thr Val Lys Leu Lys Cys Lys Glu Ser Asp Ser Pro His Ala			
430	435	440	
gtt act gta tat atg cta gag cct cac tcc tgt caa tat att ctt ggg			1396
Val Thr Val Tyr Met Leu Glu Pro His Ser Cys Gln Tyr Ile Leu Gly			
445	450	455	460
gtt gaa tct cca gtg atc tgt aaa atc tta gat aca gca gat gaa aat			1444
Val Glu Ser Pro Val Ile Cys Lys Ile Leu Asp Thr Ala Asp Glu Asn			
465	470	475	
gga ctt ctt tct ctc ccc aac taaaggatat taaagttagg ggaaa			1490
Gly Leu Leu Ser Leu Pro Asn			
480			
gaaaagatca ttgaaagtca tgataatttc tgtcccactg tgtctcatta tagagttctc			1550
agccattgga cctcttctaa aggatggtat aaaatgactc tcaaccactt tgtgaataca			1610
tatgtgtata taagagggtta ttgataaact tctgaggcag ac			1652

<210> 55

<211> 2112

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

94/233

<222> (20)...(1843)

<400> 55

attttggtgg	gtgagcagc	atg ggc ttt gag gag ctg ctg gag cag gtg ggc	52
Met Gly Phe Glu Glu Leu Leu Glu Gln Val Gly			
1	5	10	
ggc ttt ggg ccc ttc caa ctg cgg aat gtg gca ctg ctg gcc ctg ccc	100		
Gly Phe Gly Pro Phe Gln Leu Arg Asn Val Ala Leu Leu Ala Leu Pro			
15	20	25	
cga gtg ctg cta cca ctg cac ttc ctc ctg ccc atc ttc ctg gct gcc	148		
Arg Val Leu Leu Pro Leu His Phe Leu Leu Pro Ile Phe Leu Ala Ala			
30	35	40	
gtg cct gcc cac cga tgt gcc ctg ccg ggt gcc cct gcc aac ttc agc	196		
Val Pro Ala His Arg Cys Ala Leu Pro Gly Ala Pro Ala Asn Phe Ser			
45	50	55	
cat cag gat gtg tgg ctg gag gcc cat ctt ccc cgg gag cct gat ggc	244		
His Gln Asp Val Trp Leu Glu Ala His Leu Pro Arg Glu Pro Asp Gly			
60	65	70	75
acg ctc agc tcc tgc ctc cgc ttt gcc tat ccc cag gct ctc ccc aac	292		
Thr Leu Ser Ser Cys Leu Arg Phe Ala Tyr Pro Gln Ala Leu Pro Asn			
80	85	90	
acc acg ttg ggg gaa gaa agg cag agc cgt ggg gag ctg gag gat gaa	340		
Thr Thr Leu Gly Glu Glu Arg Gln Ser Arg Gly Glu Leu Glu Asp Glu			
95	100	105	
cct gcc aca gtg ccc tgc tct cag ggc tgg gag tac gac cac tca gaa	388		
Pro Ala Thr Val Pro Cys Ser Gln Gly Trp Glu Tyr Asp His Ser Glu			
110	115	120	
ttc tcc tct acc att gca act gag tcc cag gtc ggt att tac ata atc	436		
Phe Ser Ser Thr Ile Ala Thr Glu Ser Gln Val Gly Ile Tyr Ile Ile			
125	130	135	
cat ctg gag gtg gaa tgt cgg tgg agg cag tct ccc tgg gag gca gca	484		
His Leu Glu Val Glu Cys Arg Trp Arg Gln Ser Pro Trp Glu Ala Ala			
140	145	150	155
ggt cga ggc ctt cct tgg gaa gaa gct gag gct gca gga ctg ggg agg	532		
Gly Arg Gly Leu Pro Trp Glu Glu Ala Glu Ala Ala Gly Leu Gly Arg			
160	165	170	

95/233

gac aaa gtt tcc tat tcc cca agc tgg cgt gaa tcg ttg gga ggt tta	580
Asp Lys Val Ser Tyr Ser Pro Ser Trp Arg Glu Ser Leu Gly Gly Leu	
175 180 185	
tta tct ggc atg gag tgg gat ctg gtg tgt gag cag aaa ggt ctg aac	628
Leu Ser Gly Met Glu Trp Asp Leu Val Cys Glu Gln Lys Gly Leu Asn	
190 195 200	
aga gct gcg tcc act ttc ttc ttc gcc ggt gtg ctg gtg ggg gct gtg	676
Arg Ala Ala Ser Thr Phe Phe Phe Ala Gly Val Leu Val Gly Ala Val	
205 210 215	
gcc ttt gga tat ctg tcc gac agg ttt ggg cgg cgg cgt ctg ctg ctg	724
Ala Phe Gly Tyr Leu Ser Asp Arg Phe Gly Arg Arg Arg Leu Leu Leu	
220 225 230 235	
gta gcc tac gtg agt acc ctg gtg ctg ggc ctg gca tct gca gcc tcc	772
Val Ala Tyr Val Ser Thr Leu Val Leu Gly Leu Ala Ser Ala Ala Ser	
240 245 250	
gtc agc tat gta atg ttt gcc atc acc cgc acc ctt act ggc tca gcc	820
Val Ser Tyr Val Met Phe Ala Ile Thr Arg Thr Leu Thr Gly Ser Ala	
255 260 265	
ctg gct ggt ttt acc atc atc gtg atg cca ctg gag ctg gag tgg ctg	868
Leu Ala Gly Phe Thr Ile Ile Val Met Pro Leu Glu Leu Glu Trp Leu	
270 275 280	
gat gtg gag cac cgc acc gtg gct gga gtc ctg agc agc acc ttc tgg	916
Asp Val Glu His Arg Thr Val Ala Gly Val Leu Ser Ser Thr Phe Trp	
285 290 295	
aca ggg ggc gtg atg ctg ctg gca ctg gtt ggg tac ctg ata cgg gac	964
Thr Gly Gly Val Met Leu Leu Ala Leu Val Gly Tyr Leu Ile Arg Asp	
300 305 310 315	
tgg cga tgg ctt ctg cta gct gtc acc ctg cct tgt gcc cca ggc atc	1012
Trp Arg Trp Leu Leu Leu Ala Val Thr Leu Pro Cys Ala Pro Gly Ile	
320 325 330	
ctc agc ctc tgg tgg gtg cct gag tct gca cgc tgg ctt ctg acc caa	1060
Leu Ser Leu Trp Trp Val Pro Glu Ser Ala Arg Trp Leu Leu Thr Gln	
335 340 345	
ggc cat gtg aaa gag gcc cac agg tac ttg ctc cac tgt gcc agg ctc	1108
Gly His Val Lys Glu Ala His Arg Tyr Leu Leu His Cys Ala Arg Leu	

96/233

350	355	360	
aat ggg cgg cca gtg tgt gag gac agc ttc agc cag gag gct gtg agc			1156
Asn Gly Arg Pro Val Cys Glu Asp Ser Phe Ser Gln Glu Ala Val Ser			
365	370	375	
aaa gtg gcc gcc ggg gaa cgg gtg gtc cga aga cct tca tac cta gac			1204
Lys Val Ala Ala Gly Glu Arg Val Val Arg Arg Pro Ser Tyr Leu Asp			
380	385	390	395
ctg ttc cgc aca cca cgg ctc cga cac atc tca ctg tgc tgc gtg gtg			1252
Leu Phe Arg Thr Pro Arg Leu Arg His Ile Ser Leu Cys Cys Val Val			
400	405	410	
gtg tgg ttc gga gtg aac ttc tcc tat tac ggc ctg agt ctg gat gtg			1300
Val Trp Phe Gly Val Asn Phe Ser Tyr Tyr Gly Leu Ser Leu Asp Val			
415	420	425	
tcg ggg ctg ggg ctg aac gtg tac cag aca cag ctg ttg ttc ggg gct			1348
Ser Gly Leu Gly Leu Asn Val Tyr Gln Thr Gln Leu Leu Phe Gly Ala			
430	435	440	
gtg gaa ctg ccc tcc aag ctg ctg gtc tac ttg tcg gtg cgc tac gca			1396
Val Glu Leu Pro Ser Lys Leu Leu Val Tyr Leu Ser Val Arg Tyr Ala			
445	450	455	
gga cgc cgc ctc acg caa gcc ggg aca ctg ctg ggc acg gcc ctg gcg			1444
Gly Arg Arg Leu Thr Gln Ala Gly Thr Leu Leu Gly Thr Ala Leu Ala			
460	465	470	475
ttc ggc act aga ctg cta gtg tcc tct gat atg aag tcc tgg agc act			1492
Phe Gly Thr Arg Leu Leu Val Ser Ser Asp Met Lys Ser Trp Ser Thr			
480	485	490	
gtc ctg gca gtg atg ggg aaa gct ttt tct gaa gct gcc ttc acc act			1540
Val Leu Ala Val Met Gly Lys Ala Phe Ser Glu Ala Ala Phe Thr Thr			
495	500	505	
gcc tac ctg ttc act tca gag ttg tac cct acg gtg ctc aga cag aca			1588
Ala Tyr Leu Phe Thr Ser Glu Leu Tyr Pro Thr Val Leu Arg Gln Thr			
510	515	520	
ggg atg ggg ctg act gca ctg gtg ggc cgg ctg ggg ggc tct ttg gcc			1636
Gly Met Gly Leu Thr Ala Leu Val Gly Arg Leu Gly Gly Ser Leu Ala			
525	530	535	
cca ctg gcg gcc ttg ctg gat gga gtg tgg ctg tca ctg ccc aag ctt			1684

97/233

Pro Leu Ala Ala Leu Leu Asp Gly Val Trp Leu Ser Leu Pro Lys Leu
 540 545 550 555
 act tat ggg ggg atc gcc ctg ctg gct gcc ggc acc gcc ctc ctg ctg 1732
 Thr Tyr Gly Gly Ile Ala Leu Leu Ala Ala Gly Thr Ala Leu Leu Leu
 560 565 570
 cca gag acg agg cag gca cag ctg cca gag acc atc cag gac gtg gag 1780
 Pro Glu Thr Arg Gln Ala Gln Leu Pro Glu Thr Ile Gln Asp Val Glu
 575 580 585
 aga aag agt gcc cca acc agt ctt cag gag gaa gag atg ccc atg aag 1828
 Arg Lys Ser Ala Pro Thr Ser Leu Gln Glu Glu Glu Met Pro Met Lys
 590 595 600
 cag gtc cag aac taagtgggag tggaggcagg ccctccacag aagctctgca 1880
 Gln Val Gln Asn
 605
 gcaggggctg ggagagcaga agggcaggcc ctgcaactca ggctgggagt atcgaaccct 1940
 ctgcctaggg ccggagttgc tgccagtacc cgctccctct gctcatccat ccttgattat 2000
 ttggcttcta ggaacagttg acttcccaga atgcagtggg ctgctgggca cccctctcac 2060
 ggttggggag gattctgtaa ataaaggtgc cccttggggtt ggggcagtgg tg 2112

<210> 56
 <211> 1087
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (33)...(977)
 <400> 56

agagggggcg tcaggccgcg ggagaggagg cc atg ggc gcg cgc ggg gcg ctg 53
 Met Gly Ala Arg Gly Ala Leu
 1 5
 ctg ctg gcg ctg ctg ctg gct cgg gct gga ctc agg aag ccg gag tcg 101
 Leu Leu Ala Leu Leu Leu Ala Arg Ala Gly Leu Arg Lys Pro Glu Ser
 10 15 20
 cag gag gcg gcg ccg tta tca gga cca tgc ggc cga cgg gtc atc acg 149
 Gln Glu Ala Ala Pro Leu Ser Gly Pro Cys Gly Arg Arg Val Ile Thr

98/233

25	30	35	
tcg cgc atc gtg ggt gga gag gac gcc gaa ctc ggg cgt tgg ccg tgg			197
Ser Arg Ile Val Gly Gly Glu Asp Ala Glu Leu Gly Arg Trp Pro Trp			
40	45	50	55
cag ggg agc ctg cgc ctg tgg gat tcc cac gta tgc gga gtg agc ctg			245
Gln Gly Ser Leu Arg Leu Trp Asp Ser His Val Cys Gly Val Ser Leu			
60	65	70	
ctc agc cac cgc tgg gca ctc acg gcg gcg cac tgc ttt gaa acc tat			293
Leu Ser His Arg Trp Ala Leu Thr Ala Ala His Cys Phe Glu Thr Tyr			
75	80	85	
agt gac ctt agt gat ccc tcc ggg tgg atg gtc cag ttt ggc cag ctg			341
Ser Asp Leu Ser Asp Pro Ser Gly Trp Met Val Gln Phe Gly Gln Leu			
90	95	100	
act tcc atg cca tcc ttc tgg agc ctg cag gcc tac tac acc cgt tac			389
Thr Ser Met Pro Ser Phe Trp Ser Leu Gln Ala Tyr Tyr Thr Arg Tyr			
105	110	115	
ttc gta tcg aat atc tat ctg agc cct cgc tac ctg ggg aat tca ccc			437
Phe Val Ser Asn Ile Tyr Leu Ser Pro Arg Tyr Leu Gly Asn Ser Pro			
120	125	130	135
tat gac att gcc ttg gtg aag ctg tct gca cct gtc acc tac act aaa			485
Tyr Asp Ile Ala Leu Val Lys Leu Ser Ala Pro Val Thr Tyr Thr Lys			
140	145	150	
cac atc cag ccc atc tgt ctc cag gcc tcc aca ttt gag ttt gag aac			533
His Ile Gln Pro Ile Cys Leu Gln Ala Ser Thr Phe Glu Phe Glu Asn			
155	160	165	
cgg aca gac tgc tgg gtg act ggc tgg ggg tac atc aaa gag gat gag			581
Arg Thr Asp Cys Trp Val Thr Gly Trp Gly Tyr Ile Lys Glu Asp Glu			
170	175	180	
gca ctg cca tct ccc cac acc ctc cag gaa gtt cag gtc gcc atc ata			629
Ala Leu Pro Ser Pro His Thr Leu Gln Glu Val Gln Val Ala Ile Ile			
185	190	195	
aac aac tct atg tgc aac cac ctc ttc ctc aag tac agt ttc cgc aag			677
Asn Asn Ser Met Cys Asn His Leu Phe Leu Lys Tyr Ser Phe Arg Lys			
200	205	210	215
gac atc ttt gga gac atg gtt tgt gct ggc aat gcc caa ggc ggg aag			725

Asp	Ile	Phe	Gly	Asp	Met	Val	Cys	Ala	Gly	Asn	Ala	Gln	Gly	Gly	Lys
220							225					230			
gat	gcc	tgc	ttc	ggg	gac	tca	ggg	gga	ccc	ttg	gcc	tgt	aac	aag	aat
773															
Asp	Ala	Cys	Phe	Gly	Asp	Ser	Gly	Gly	Pro	Leu	Ala	Cys	Asn	Lys	Asn
235							240					245			
gga	ctg	tgg	tat	cag	att	gga	gtc	gtg	agc	tgg	gga	gtg	ggc	tgt	ggg
821															
Gly	Leu	Trp	Tyr	Gln	Ile	Gly	Val	Val	Ser	Trp	Gly	Val	Gly	Cys	Gly
250							255					260			
cgg	ccc	aat	cgg	ccc	ggg	gtc	tac	acc	aat	atc	agc	cac	cac	ttt	gag
869															
Arg	Pro	Asn	Arg	Pro	Gly	Val	Tyr	Thr	Asn	Ile	Ser	His	His	Phe	Glu
265							270					275			
tgg	atc	cag	aag	ctg	atg	gcc	cag	agt	ggc	atg	tcc	cag	cca	gac	ccc
917															
Trp	Ile	Gln	Lys	Leu	Met	Ala	Gln	Ser	Gly	Met	Ser	Gln	Pro	Asp	Pro
280							285					290			
												295			
tcc	tgg	ccg	cta	ctc	ttt	ttc	cct	ctt	ctc	tgg	ggt	ctc	cca	ctc	ctg
965															
Ser	Trp	Pro	Leu	Leu	Phe	Phe	Pro	Leu	Leu	Trp	Ala	Leu	Pro	Leu	Leu
300							305					310			
ggg	ccg	gtc	tgagcctacc	tgagcccatg	cagcctggggg	ccactgccaa	gtcagg								
1020															
Gly	Pro	Val													

ccctggttct cttctgtctt gtttggtaat aaacacattc cagttgatgc cttgcagggc 1080
attcttc 1087

<400> 57

cccgaaagttt	gaggggtgtg	gacggtttgt	gacccctta	gcgacccta	ctctcactg	60
gccgggacaa	ctggtcttat	cacggaggct	ggggccaggc	agcccttcgg	ttcgggtggg	120
cccatggacc	ccagtccaac	gccgagggaa	taggaccatc	caaaagcgga	accttcgcct	180
cagaaaaagg	cgtggacctt	gccagcagcc	aggcc	atg gag ctc tct gat gtc		233

100/233

										Met	Glu	Leu	Ser	Asp	Val	
										1					5	
acc	ctc	att	gag	ggt	gtg	ggt	aat	gag	gtg	atg	gtg	gtg	gca	ggt	gtg	281
Thr	Leu	Ile	Glu	Gly	Val	Gly	Asn	Glu	Val	Met	Val	Val	Ala	Gly	Val	
										10		15		20		
gtg	gtg	ctg	att	cta	gcc	ttg	gtc	cta	gct	tgg	ctc	tct	acc	tac	gta	329
Val	Val	Leu	Ile	Leu	Ala	Leu	Val	Leu	Ala	Trp	Leu	Ser	Thr	Tyr	Val	
										25		30		35		
gca	gac	agc	ggt	agc	aac	cag	ctc	ctg	ggc	gct	att	gtg	tca	gca	ggc	377
Ala	Asp	Ser	Gly	Ser	Asn	Gln	Leu	Leu	Gly	Ala	Ile	Val	Ser	Ala	Gly	
										40		45		50		
gac	aca	tcc	gtc	ctc	cac	ctg	ggg	cat	gtg	gac	cac	ctg	gtg	gca	ggc	425
Asp	Thr	Ser	Val	Leu	His	Leu	Gly	His	Val	Asp	His	Leu	Val	Ala	Gly	
										55		60		65		
caa	ggc	aac	ccc	gag	cca	act	gaa	ctc	ccc	cat	cca	tca	gag	gca	aat	473
Gln	Gly	Asn	Pro	Glu	Pro	Thr	Glu	Leu	Pro	His	Pro	Ser	Glu	Ala	Asn	
										75		80		85		
act	tcc	ctg	gac	aag	aaa	gcc	aga	tga	aactgat	ctaccagggc	cgc	520				
Thr	Ser	Leu	Asp	Lys	Lys	Ala	Arg									
										90						
ctgctacaag	accagccccg	cacactgcgt	tctctgaaca	ttaccgacaa	ctgtgtgatt	580										
cactgccacc	gctcaccccc	agggtcagct	gttcaggcc	cctcagcctc	cttgccccc	640										
tcggccactg	agccaccag	ccttggtgtc	aatgtgggca	gcctcatggt	gcctgtcttt	700										
gtggtgctgt	tgggtgtggt	ctggtacttc	cgaatcaatt	accgccaatt	cttcacagca	760										
cctgccactg	tctccctggt	gggagtcacc	gtcttcttca	gcttcctagt	atttgggatg	820										
tatggacgat	aaggacatag	gaagaaaatg	aaaggcatgg	tctttctcct	ttatggcctc	880										
cccacttttc	ctggccagag	ctgggcccac	gggcccggga	gggaggggtg	gaaaggatgt	940										
gatggaaaac	tctccatag	gacacaggag	gcaagtatgc	ggcctccct	tctcatccac	1000										
aggagtacag	atgtccctcc	cgtgcgagca	caactcaggt	agaaatgagg	atgtcatctt	1060										
ccttcacttt	tagggtcctc	tgaaggagtt	caaagctgct	ggccaagctc	agtggggagc	1120										
ctgggctctg	agattccctc	ccacctgtgg	ttctgactct	tcccagtgtc	ctgcatgtct	1180										
gccccagca	cccagggtg	cctgcaagg	cagctcagca	tggccccagc	acaactccgt	1240										
agggagcctg	gagtatcctt	ccatttctca	gcccataact	catcttttga	gactgaaatc	1300										
acactggcgg	gaatgaagat	tgtgccagcc	ttctcttatg	ggcacctagc	cgccttcacc	1360										
ttcttctct	acccttagc	aggaatagg	tgtcctccct	tctttcaaag	cactttgctt	1420										

101/233

gcatttttatt ttattttttt aagagtoctt catagagctc agtcaggaag gggatggggc 1480
 accaagccaa gccccagca ttgggagcgg ccaggccaca gctgctgctc ccgtagtcct 1540
 caggctgtaa gcaagagaca gcaactggccc ttggccagcg tcctaccctg cccaactcca 1600
 aggactgggt atggattgct gggccctagg ctcttgcttc tggggctatt ggagggtcag 1660
 tgtctgtgac tgaataaagt tccattttgt ggtc 1694

<210> 58

<211> 1522

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (12)...(668)

<400> 58

cctttcccaa g atg gcg tcg aag ata ggt tcg aga cgg tgg atg ttg cag 50
 Met Ala Ser Lys Ile Gly Ser Arg Arg Trp Met Leu Gln
 1 5 10
 ctg atc atg cag ttg ggt tcg gtg ctg ctc aca cgc tgc ccc ttt tgg 98
 Leu Ile Met Gln Leu Gly Ser Val Leu Leu Thr Arg Cys Pro Phe Trp
 15 20 25
 ggc tgc ttc agc cag ctc atg ctg tac gct gag agg gct gag gca cgc 146
 Gly Cys Phe Ser Gln Leu Met Leu Tyr Ala Glu Arg Ala Glu Ala Arg
 30 35 40 45
 cgg aag ccc gac atc cca gtg cct tac ctg tat ttc gac atg ggg gca 194
 Arg Lys Pro Asp Ile Pro Val Pro Tyr Leu Tyr Phe Asp Met Gly Ala
 50 55 60
 gcc gtg ctg tgc gct agt ttc atg tcc ttt ggc gtg aag cgg cgc tgg 242
 Ala Val Leu Cys Ala Ser Phe Met Ser Phe Gly Val Lys Arg Arg Trp
 65 70 75
 ttc gcg ctg ggg gcc gca ctc caa ttg gcc att agc acc tac gcc gcc 290
 Phe Ala Leu Gly Ala Ala Leu Gln Leu Ala Ile Ser Thr Tyr Ala Ala
 80 85 90
 tac atc ggg ggc tac gtc cac tac ggg gac tgg ctg aag gtc cgt atg 338
 Tyr Ile Gly Gly Tyr Val His Tyr Gly Asp Trp Leu Lys Val Arg Met
 95 100 105

102/233

tac tcg cgc aca gtt gcc atc atc ggc gga ctt tct tgt gtt ggc cag	386
Tyr Ser Arg Thr Val Ala Ile Ile Gly Gly Leu Ser Cys Val Gly Gln	
110 115 120 125	
cgg tgc tgg gga gct gta ccg ccg gaa acc tcg cag ccg ctc cct gca	434
Arg Cys Trp Gly Ala Val Pro Pro Glu Thr Ser Gln Pro Leu Pro Ala	
130 135 140	
gtc cac cgg cca ggt gtt cct ggg tat cta cct cat ctg tgt ggc cta	482
Val His Arg Pro Gly Val Pro Gly Tyr Leu Pro His Leu Cys Gly Leu	
145 150 155	
ctc act gca gca cag caa gga gga ccg gct ggc gta tct gaa cca tct	530
Leu Thr Ala Ala Gln Gln Gly Gly Pro Ala Gly Val Ser Glu Pro Ser	
160 165 170	
ccc agg agg gga gct gat gat cca gct gtt ctt cgt gct gta tgg cat	578
Pro Arg Arg Gly Ala Asp Asp Pro Ala Val Leu Arg Ala Val Trp His	
175 180 185	
cct ggc cct ggc ctt tct gtc agg cta cta cgt gac cct cgc tgc cca	626
Pro Gly Pro Gly Leu Ser Val Arg Leu Leu Arg Asp Pro Arg Cys Pro	
190 195 200 205	
gat cct ggc tgt act gct gcc ccc tgt cat gct gct cat tgatg	670
Asp Pro Gly Cys Thr Ala Ala Pro Cys His Ala Ala His	
210 215	
gcaatgttgc ttactggcac aacacggcgc gtgttgagtt ctggaaccag atgaagetcc	730
ttggagagag tgtgggcac ttcggaactg ctgtcatctg gccactgatg gctgagtttt	790
atggcaagag gctgagatgg gcacagggag ccaactgaggg tcaccctgcc ttcctccttg	850
ctggcccage tgetgtttat ttatgctttt tggctctgttt gtttgatctt ttgctttttt	910
aaaattgttt ttgcagtta agaggcagct catttgtcca aatttctggg ctcagcgctt	970
gggagggcag gagccctggc actaatgctg tacaggtttt tttcctgtta ggagagctga	1030
ggccagctgc ccaactgagtc tcctgtccct gagaaggagg tatggcaggg ctgggatgcg	1090
gctactgaga gtgggagagt gggagacaga ggaagggaaga tggagattgg aagtgagcaa	1150
atgtgaaaaa ttcctctttg aacctggcag atgcagctag gctctgcagt gctgtttgga	1210
gactgtgaga gggagtgcgt gtgttgacac atgtggatca ggcccaggaa gggcacaggg	1270
gctgagcact acagaagtca catgggttct cagggtatgc caggggcaga aacagtaccg	1330
gctctctgtc actcaccttg agagtagagc agacctgtt ctgctctggg ctgtgaaggg	1390
gtggagcagg cagtggccag ctttgccctt cctgctgtct ctgtttctag ctccatggtt	1450
ggcctggtgg ggggtggagt cctcccaaa caccagacca cacagtcctc caaaaataaa	1510

103/233

cattttatat ag

1522

<210> 59

<211> 1591

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (44)...(1426)

<400> 59

gaaaacagtt ccacgttgct tgaaattgaa aatcaagata aaa atg ttc aca att 55

Met Phe Thr Ile

1

aag ctc ctt ctt ttt att gtt cct cta gtt att tcc tcc aga att gat 103

Lys Leu Leu Leu Phe Ile Val Pro Leu Val Ile Ser Ser Arg Ile Asp

5

10

15

20

caa gac aat tca tca ttt gat tct cta tct cca gag cca aaa tca aga 151

Gln Asp Asn Ser Ser Phe Asp Ser Leu Ser Pro Glu Pro Lys Ser Arg

25

30

35

ttt gct atg tta gac gat gta aaa att tta gcc aat ggc ctc ctt cag 199

Phe Ala Met Leu Asp Asp Val Lys Ile Leu Ala Asn Gly Leu Leu Gln

40

45

50

ttg gga cat ggt ctt aaa gac ttt gtc cat aag acg aag ggc caa att 247

Leu Gly His Gly Leu Lys Asp Phe Val His Lys Thr Lys Gly Gln Ile

55

60

65

aat gac ata ttt caa aaa ctc aac ata ttt gat cag tct ttt tat gat 295

Asn Asp Ile Phe Gln Lys Leu Asn Ile Phe Asp Gln Ser Phe Tyr Asp

70

75

80

cta tcg ctg caa acc agt gaa atc aaa gaa gaa gaa aag gaa ctg aga 343

Leu Ser Leu Gln Thr Ser Glu Ile Lys Glu Glu Glu Lys Glu Leu Arg

85

90

95

100

aga act aca tat aaa cta caa gtc aaa aat gaa gag gta aag aat atg 391

Arg Thr Thr Tyr Lys Leu Gln Val Lys Asn Glu Glu Val Lys Asn Met

105

110

115

tca ctt gaa ctc aac tca aaa ctt gaa agc ctc cta gaa gaa aaa att 439

104/233

Ser Leu Glu Leu Asn Ser Lys Leu Glu Ser Leu Leu Glu Glu Lys Ile	
120	125 130
cta ctt caa caa aaa gtg aaa tat tta gaa gag caa cta act aac tta	487
Leu Leu Gln Gln Lys Val Lys Tyr Leu Glu Glu Gln Leu Thr Asn Leu	
135	140 145
att caa aat caa cct gaa act cca gaa cac cca gaa gta act tca ctt	535
Ile Gln Asn Gln Pro Glu Thr Pro Glu His Pro Glu Val Thr Ser Leu	
150	155 160
aaa act ttt gta gaa aaa caa gat aat agc atc aaa gac ctt ctc cag	583
Lys Thr Phe Val Glu Lys Gln Asp Asn Ser Ile Lys Asp Leu Leu Gln	
165	170 175 180
acc gtg gaa gac caa tat aaa caa tta aac caa cag cat agt caa ata	631
Thr Val Glu Asp Gln Tyr Lys Gln Leu Asn Gln Gln His Ser Gln Ile	
185	190 195
aaa gaa ata gaa aat cag ctc aga agg act agt att caa gaa ccc aca	679
Lys Glu Ile Glu Asn Gln Leu Arg Arg Thr Ser Ile Gln Glu Pro Thr	
200	205 210
gaa att tct cta tct tcc aag cca aga gca cca aga act act ccc ttt	727
Glu Ile Ser Leu Ser Ser Lys Pro Arg Ala Pro Arg Thr Thr Pro Phe	
215	220 225
ctt cag ttg aat gaa ata aga aat gta aaa cat gat ggc att cct gct	775
Leu Gln Leu Asn Glu Ile Arg Asn Val Lys His Asp Gly Ile Pro Ala	
230	235 240
gaa tgt acc acc att tat aac aga ggt gaa cat aca agt ggc atg tat	823
Glu Cys Thr Thr Ile Tyr Asn Arg Gly Glu His Thr Ser Gly Met Tyr	
245	250 255 260
gcc atc aga ccc agc aac tct caa gtt ttt cat gtc tac tgt gat gtt	871
Ala Ile Arg Pro Ser Asn Ser Gln Val Phe His Val Tyr Cys Asp Val	
265	270 275
ata tca ggt agt cca tgg aca tta att caa cat cga ata gat gga tca	919
Ile Ser Gly Ser Pro Trp Thr Leu Ile Gln His Arg Ile Asp Gly Ser	
280	285 290
caa aac ttc aat gaa acg tgg gag aac tac aaa tat ggt ttt ggg agg	967
Gln Asn Phe Asn Glu Thr Trp Glu Asn Tyr Lys Tyr Gly Phe Gly Arg	
295	300 305

105/233

ctt gat gga gaa ttt tgg ttg ggc cta gag aag ata tac tcc ata gtg 1015
 Leu Asp Gly Glu Phe Trp Leu Gly Leu Glu Lys Ile Tyr Ser Ile Val
 310 315 320
 aag caa tct aat tat gtt tta cga att gag ctg gaa gac tgg aaa gac 1063
 Lys Gln Ser Asn Tyr Val Leu Arg Ile Glu Leu Glu Asp Trp Lys Asp
 325 330 335 340
 aac aaa cat tat att gaa tat tct ttt tac ttg gga aat cac gaa acc 1111
 Asn Lys His Tyr Ile Glu Tyr Ser Phe Tyr Leu Gly Asn His Glu Thr
 345 350 355
 aac tat acg cta cat cta gtt gcg att act ggc aat gtc ccc aat gca 1159
 Asn Tyr Thr Leu His Leu Val Ala Ile Thr Gly Asn Val Pro Asn Ala
 360 365 370
 atc ccg gaa aac aaa gat ttg gtg ttt tct act tgg gat cac aaa gca 1207
 Ile Pro Glu Asn Lys Asp Leu Val Phe Ser Thr Trp Asp His Lys Ala
 375 380 385
 aaa gga cac ttc aac tgt cca gag ggt tat tca gga ggc tgg tgg tgg 1255
 Lys Gly His Phe Asn Cys Pro Glu Gly Tyr Ser Gly Gly Trp Trp Trp
 390 395 400
 cat gat gag tgt gga gaa aac aac cta aat ggt aaa tat aac aaa cca 1303
 His Asp Glu Cys Gly Glu Asn Asn Leu Asn Gly Lys Tyr Asn Lys Pro
 405 410 415 420
 aga gca aaa tct aag cca gag agg aga aga gga tta tct tgg aag tct 1351
 Arg Ala Lys Ser Lys Pro Glu Arg Arg Arg Gly Leu Ser Trp Lys Ser
 425 430 435
 caa aat gga agg tta tac tct ata aaa tca acc aaa atg ttg atc cat 1399
 Gln Asn Gly Arg Leu Tyr Ser Ile Lys Ser Thr Lys Met Leu Ile His
 440 445 450
 cca aca gat tca gaa agc ttt gaa tgaactgagg caaatttaaa aggcaat 1450
 Pro Thr Asp Ser Glu Ser Phe Glu
 455 460
 aatttaaaaca ttaacctcat tocaagttaa tgtggtotaa taatctggta ttaaatoctt 1510
 aagagaaagc ttgagaaata gatttttttt tatcttaaaag tcaactgtota ttttaagatta 1570
 aacataacaat cacataacct t 1591

<210> 60

106/233

<211> 1249

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (134)...(784)

<400> 60

```

aacagtctgt ggagacagtt gtgtccctgt ggctttggtg cgctgtgtg cactttctcc      60
ctccacctgg agcatgggct aacaccggag gaaaggaaaa gacagagtca gacagggagc      120
ctggggaggg gcc atg gtg cca atg cac tta ctg ggg aga ctg gag aag      169
      Met Val Pro Met His Leu Leu Gly Arg Leu Glu Lys
              1              5              10
ccg ctt ctc ctc ctg tgc tgc gcc tcc ttc cta ctg ggg ctg gct ttg      217
Pro Leu Leu Leu Leu Cys Cys Ala Ser Phe Leu Leu Gly Leu Ala Leu
      15              20              25
ctg ggc ata aag acg gac atc acc ccc gtt gct tat ttc ttt ctc aca      265
Leu Gly Ile Lys Thr Asp Ile Thr Pro Val Ala Tyr Phe Phe Leu Thr
      30              35              40
ttg ggt ggc ttc ttc ttg ttt gcc tat ctc ctg gtc cgg ttt ctg gaa      313
Leu Gly Gly Phe Phe Leu Phe Ala Tyr Leu Leu Val Arg Phe Leu Glu
      45              50              55              60
tgg ggg ctt cgg tcc cag ctc caa tca atg cag act gag agc cca ggg      361
Trp Gly Leu Arg Ser Gln Leu Gln Ser Met Gln Thr Glu Ser Pro Gly
      65              70              75
ccc tca ggc aat gca cgg gac aat gaa gcc ttt gaa gtg cca gtc tat      409
Pro Ser Gly Asn Ala Arg Asp Asn Glu Ala Phe Glu Val Pro Val Tyr
      80              85              90
gaa gag gcc gtg gtg gga cta gaa tcc cag tgc cgc ccc caa gag ttg      457
Glu Glu Ala Val Val Gly Leu Glu Ser Gln Cys Arg Pro Gln Glu Leu
      95              100              105
gac caa cca ccc ccc tac agc act gtt gtg ata ccc cca gca cct gag      505
Asp Gln Pro Pro Pro Tyr Ser Thr Val Val Ile Pro Pro Ala Pro Glu
      110              115              120
gag gaa caa cct agc cat cca gag ggg tcc agg aga gcc aaa ctg gaa      553
Glu Glu Gln Pro Ser His Pro Glu Gly Ser Arg Arg Ala Lys Leu Glu

```

107/233

125	130	135	140	
cag agg cga atg gcc tca gag ggg tcc atg gcc cag gaa gga agc cct				601
Gln Arg Arg Met Ala Ser Glu Gly Ser Met Ala Gln Glu Gly Ser Pro				
	145	150	155	
gga aga gct cca atc aac ctt cgg ctt cgg gga cca cgg gct gtg tcc				649
Gly Arg Ala Pro Ile Asn Leu Arg Leu Arg Gly Pro Arg Ala Val Ser				
	160	165	170	
act gct cct gat ctg cag agc ttg gcg gca gtc ccc aca tta gag cct				697
Thr Ala Pro Asp Leu Gln Ser Leu Ala Ala Val Pro Thr Leu Glu Pro				
	175	180	185	
ctg act cca ccc cct gcc tat gat gtc tgc ttt ggt cac cct gat gat				745
Leu Thr Pro Pro Pro Ala Tyr Asp Val Cys Phe Gly His Pro Asp Asp				
	190	195	200	
gat agt gtt ttt tat gag gac aac tgg gca ccc cct taaatgact				790
Asp Ser Val Phe Tyr Glu Asp Asn Trp Ala Pro Pro				
205	210	215		
ctcccaagat ttctcttctc tccacaccag acctcgttca tttgactaac attttccagc				850
gcctactatg tgtcagaaac aagtgtttct gcctggacat cataaatggg gacttggacc				910
ctgaggagag tcaggccacg gtaagccctt cccagctgag atatgggtgg cataatttga				970
gtctcttgge aacatttggt gacctacccc atatccaata tttccagcgt tagattgagg				1030
atgaggtagg gaggtgatcc agagaaggcg gagaaggaag aagtaacctc tgagtggcgg				1090
ctattgcttc tgttccaggt gctgttcgag ctgttagaac ccttaggctt gacagctttg				1150
tgagttatta ttgaaaaatg aggattccaa gagtcagagg agtttgataa tgtgcacgag				1210
ggcacactgc tagtaaataa cattaaaata actggaatg				1249

<210> 61

<211> 392

<212> PRT

<213> Homo sapiens

<400> 61

Met Glu Gly Val Ser Ala Leu Leu Ala Arg Cys Pro Thr Ala Gly Leu

1

5

10

15

Ala Gly Gly Leu Gly Val Thr Ala Cys Ala Ala Ala Gly Val Leu Leu

20

25

30

Tyr Arg Ile Ala Arg Arg Met Lys Pro Thr His Thr Met Val Asn Cys

108/233

35	40	45
Trp Phe Cys Asn Gln Asp Thr Leu Val Pro Tyr Gly Asn Arg Asn Cys		
50	55	60
Trp Asp Cys Pro His Cys Glu Gln Tyr Asn Gly Phe Gln Glu Asn Gly		
65	70	75
Asp Tyr Asn Lys Pro Ile Pro Ala Gln Tyr Leu Glu His Leu Asn His		
85	90	95
Val Val Ser Ser Ala Pro Ser Leu Arg Asp Pro Ser Gln Pro Gln Gln		
100	105	110
Trp Val Ser Ser Gln Val Leu Leu Cys Lys Arg Cys Asn His His Gln		
115	120	125
Thr Thr Lys Ile Lys Gln Leu Ala Ala Phe Ala Pro Arg Glu Glu Gly		
130	135	140
Arg Tyr Asp Glu Glu Val Glu Val Tyr Arg His His Leu Glu Gln Met		
145	150	155
Tyr Lys Leu Cys Arg Pro Cys Gln Ala Ala Val Glu Tyr Tyr Ile Lys		
165	170	175
His Gln Asn Arg Gln Leu Arg Ala Leu Leu Leu Ser His Gln Phe Lys		
180	185	190
Arg Arg Glu Ala Asp Gln Thr His Ala Gln Asn Phe Ser Ser Ala Val		
195	200	205
Lys Ser Pro Val Gln Val Ile Leu Leu Arg Ala Leu Ala Phe Leu Ala		
210	215	220
Cys Ala Phe Leu Leu Thr Thr Ala Leu Tyr Gly Ala Ser Gly His Phe		
225	230	235
Ala Pro Gly Thr Thr Val Pro Leu Ala Leu Pro Pro Gly Gly Asn Gly		
245	250	255
Ser Ala Thr Pro Asp Asn Gly Thr Thr Pro Gly Ala Glu Gly Trp Arg		
260	265	270
Gln Leu Leu Gly Leu Leu Pro Glu His Met Ala Glu Lys Leu Cys Glu		
275	280	285
Ala Trp Ala Phe Gly Gln Ser His Gln Thr Gly Val Val Ala Leu Gly		
290	295	300
Leu Leu Thr Cys Leu Leu Ala Met Leu Leu Ala Gly Arg Ile Arg Leu		
305	310	315
		320

109/233

```
<210> 62
<211> 497
<212> PRT
<213> Homo sapiens
<400> 62
```

Met Ala Leu Trp Arg Gly Ser Ala Tyr Ala Gly Phe Leu Ala Leu Ala
1 5 10 15
Val Gly Cys Val Phe Leu Leu Glu Pro Glu Leu Pro Gly Ser Ala Leu
20 25 30
Arg Ser Leu Trp Ser Ser Leu Cys Leu Gly Pro Ala Pro Ala Pro Pro
35 40 45
Gly Pro Val Ser Pro Glu Gly Arg Leu Ala Ala Ala Trp Asp Ala Leu
50 55 60
Ile Val Arg Pro Val Arg Arg Trp Arg Arg Val Ala Val Gly Val Asn
65 70 75 80
Ala Cys Val Asp Val Val Leu Ser Gly Val Lys Leu Leu Gln Ala Leu
85 90 95
Gly Leu Ser Pro Gly Asn Gly Lys Asp His Ser Ile Leu His Ser Arg
100 105 110
Asn Asp Leu Glu Glu Ala Phe Ile His Phe Met Trp Lys Gly Ala Ala
115 120 125
Ala Glu Arg Phe Phe Ser Asp Lys Glu Thr Phe His Asp Ile Ala Gln
130 135 140
Val Ala Ser Glu Phe Pro Gly Ala Gln His Tyr Val Gly Gly Asn Ala

110/233

145 150 155 160
 Ala Leu Ile Gly Gln Lys Phe Ala Ala Asn Ser Asp Leu Lys Val Leu
 165 170 175
 Leu Cys Gly Pro Val Gly Pro Arg Leu His Glu Leu Leu Asp Asp Asn
 180 185 190
 Val Phe Val Pro Pro Glu Ser Leu Gln Glu Val Asp Glu Phe His Leu
 195 200 205
 Ile Leu Glu Tyr Gln Ala Gly Glu Glu Trp Gly Gln Leu Lys Ala Pro
 210 215 220
 His Ala Asn Arg Phe Ile Phe Ser His Asp Leu Ser Asn Gly Ala Met
 225 230 235 240
 Asn Met Leu Glu Val Phe Val Ser Ser Leu Glu Glu Phe Gln Pro Asp
 245 250 255
 Leu Val Val Leu Ser Gly Leu His Met Met Glu Gly Gln Ser Lys Glu
 260 265 270
 Leu Gln Arg Lys Arg Leu Leu Glu Val Val Thr Ser Ile Ser Asp Ile
 275 280 285
 Pro Thr Gly Ile Pro Val His Leu Glu Leu Ala Ser Met Thr Asn Arg
 290 295 300
 Glu Leu Met Ser Ser Ile Val His Gln Gln Val Phe Pro Ala Val Thr
 305 310 315 320
 Ser Leu Gly Leu Asn Glu Gln Glu Leu Leu Phe Leu Thr Gln Ser Ala
 325 330 335
 Ser Gly Pro His Ser Ser Leu Ser Ser Trp Asn Gly Val Pro Asp Val
 340 345 350
 Gly Met Val Ser Asp Ile Leu Phe Trp Ile Leu Lys Glu His Gly Arg
 355 360 365
 Ser Lys Ser Arg Ala Ser Asp Leu Thr Arg Ile His Phe His Thr Leu
 370 375 380
 Val Tyr His Ile Leu Ala Thr Val Asp Gly His Trp Ala Asn Gln Leu
 385 390 395 400
 Ala Ala Val Ala Ala Gly Ala Arg Val Ala Gly Thr Gln Ala Cys Ala
 405 410 415
 Thr Glu Thr Ile Asp Thr Ser Arg Val Ser Leu Arg Ala Pro Gln Glu
 420 425 430

111/233

Phe Met Thr Ser His Ser Glu Ala Gly Ser Arg Ile Val Leu Asn Pro
 435 440 445
 Asn Lys Pro Val Val Glu Trp His Arg Glu Gly Ile Ser Phe His Phe
 450 455 460
 Thr Pro Val Leu Val Cys Lys Asp Pro Ile Arg Thr Val Gly Leu Gly
 465 470 475 480
 Asp Ala Ile Ser Ala Glu Gly Leu Phe Tyr Ser Glu Val His Pro His
 485 490 495

Tyr

<210> 63

<211> 417

<212> PRT

<213> Homo sapiens

<400> 63

Met Leu Val His Leu Phe Arg Val Gly Ile Arg Gly Gly Pro Phe Pro
 1 5 10 15
 Gly Arg Leu Leu Pro Pro Leu Arg Phe Gln Thr Phe Ser Ala Val Arg
 20 25 30
 Tyr Ser Asp Gly Tyr Arg Ser Ser Ser Leu Leu Arg Ala Val Ala His
 35 40 45
 Leu Arg Ser Gln Leu Trp Ala His Leu Pro Arg Ala Pro Leu Ala Pro
 50 55 60
 Arg Trp Ser Pro Ser Ala Trp Cys Trp Val Gly Gly Ala Leu Leu Gly
 65 70 75 80
 Pro Met Val Leu Ser Lys His Pro His Leu Cys Leu Val Ala Leu Cys
 85 90 95
 Glu Ala Glu Glu Ala Pro Pro Ala Ser Ser Thr Pro His Val Val Gly
 100 105 110
 Ser Arg Phe Asn Trp Lys Leu Phe Trp Gln Phe Leu His Pro His Leu
 115 120 125
 Leu Val Leu Gly Val Ala Val Val Leu Ala Leu Gly Ala Ala Leu Val
 130 135 140
 Asn Val Gln Ile Pro Leu Leu Leu Gly Gln Leu Val Glu Val Val Ala
 145 150 155 160

112/233

Lys Tyr Thr Arg Asp His Val Gly Ser Phe Met Thr Glu Ser Gln Asn
 165 170 175
 Leu Ser Thr His Leu Leu Ile Leu Tyr Gly Val Gln Gly Leu Leu Thr
 180 185 190
 Phe Gly Tyr Leu Val Leu Leu Ser His Val Gly Glu Arg Met Ala Val
 195 200 205
 Asp Met Arg Arg Ala Leu Phe Ser Ser Leu Leu Arg Tyr Cys Gln Pro
 210 215 220
 Gln Gly Ala Glu Leu Gly Gln Asp Ile Thr Phe Phe Asp Ala Asn Lys
 225 230 235 240
 Thr Gly Gln Leu Val Ser Arg Leu Thr Thr Asp Val Gln Glu Phe Lys
 245 250 255
 Ser Ser Phe Lys Leu Val Ile Ser Gln Gly Leu Arg Ser Cys Thr Gln
 260 265 270
 Val Ala Gly Cys Leu Val Ser Leu Ser Met Leu Ser Thr Arg Leu Thr
 275 280 285
 Leu Leu Leu Met Val Ala Thr Pro Ala Leu Met Gly Val Gly Thr Leu
 290 295 300
 Met Gly Ser Gly Leu Arg Lys Leu Ser Cys Gln Cys Gln Glu Gln Ile
 305 310 315 320
 Ala Arg Ala Met Gly Val Ala Asp Glu Ala Leu Gly Asn Val Arg Thr
 325 330 335
 Val Arg Ala Phe Ala Met Glu Gln Arg Glu Glu Glu Arg Tyr Gly Ala
 340 345 350
 Glu Leu Glu Ala Cys Arg Cys Arg Ala Glu Glu Leu Gly Arg Gly Ile
 355 360 365
 Ala Leu Phe Gln Gly Leu Ser Asn Ile Ala Phe Asn Cys Met Val Leu
 370 375 380
 Gly Thr Leu Phe Ile Gly Gly Ser Leu Val Ala Gly Gln Gln Leu Thr
 385 390 395 400
 Gly Gly Asp Leu Met Ser Phe Leu Val Ala Ser Gln Thr Val Gln Arg
 405 410 415
 Leu

113/233

<211> 649

<212> PRT

<213> Homo sapiens

<400> 64

Met Ile Pro Asn Gln His Asn Ala Gly Ala Gly Ser His Gln Pro Ala
 1 5 10 15
 Val Phe Arg Met Ala Val Leu Asp Thr Asp Leu Asp His Ile Leu Pro
 20 25 30
 Ser Ser Val Leu Pro Pro Phe Trp Ala Lys Leu Val Val Gly Ser Val
 35 40 45
 Ala Ile Val Cys Phe Ala Arg Ser Tyr Asp Gly Asp Phe Val Phe Asp
 50 55 60
 Asp Ser Glu Ala Ile Val Asn Asn Lys Val Ala Gly Val Val Gly Arg
 65 70 75 80
 Ala Asp Leu Leu Cys Ala Leu Phe Phe Leu Leu Ser Phe Leu Gly Tyr
 85 90 95
 Cys Lys Ala Phe Arg Glu Ser Asn Lys Glu Gly Ala His Ser Ser Thr
 100 105 110
 Phe Trp Val Leu Leu Ser Ile Phe Leu Gly Ala Val Ala Met Leu Cys
 115 120 125
 Lys Glu Gln Gly Ile Thr Val Leu Gly Leu Asn Ala Val Phe Asp Ile
 130 135 140
 Leu Val Ile Gly Lys Phe Asn Val Leu Glu Ile Val Gln Lys Val Leu
 145 150 155 160
 His Lys Asp Lys Ser Leu Glu Asn Leu Gly Met Leu Arg Asn Gly Gly
 165 170 175
 Leu Leu Phe Arg Met Thr Leu Leu Thr Ser Gly Gly Ala Gly Met Leu
 180 185 190
 Tyr Val Arg Trp Arg Ile Met Gly Thr Gly Pro Pro Ala Phe Thr Glu
 195 200 205
 Val Asp Asn Pro Ala Ser Phe Ala Asp Ser Met Leu Val Arg Ala Val
 210 215 220
 Asn Tyr Asn Tyr Tyr Tyr Ser Leu Asn Ala Trp Leu Leu Leu Cys Pro
 225 230 235 240
 Trp Trp Leu Cys Phe Asp Trp Ser Met Gly Cys Ile Pro Leu Ile Lys

114/233

245	250	255
Ser Ile Ser Asp Trp Arg Val Ile Ala Leu Ala Ala Leu Trp Phe Cys		
260	265	270
Leu Ile Gly Leu Ile Cys Gln Ala Leu Cys Ser Glu Asp Gly His Lys		
275	280	285
Arg Arg Ile Leu Thr Leu Gly Leu Gly Phe Leu Val Ile Pro Phe Leu		
290	295	300
Pro Ala Ser Asn Leu Phe Phe Arg Val Gly Phe Val Val Ala Glu Arg		
305	310	315
Val Leu Tyr Leu Pro Ser Ile Gly Tyr Cys Val Leu Leu Thr Phe Gly		
325	330	335
Phe Gly Ala Leu Ser Lys His Thr Lys Lys Lys Lys Leu Ile Ala Ala		
340	345	350
Val Val Leu Gly Ile Leu Phe Ile Asn Thr Leu Arg Cys Val Leu Arg		
355	360	365
Ser Gly Glu Trp Arg Ser Glu Glu Gln Leu Phe Arg Ser Ala Leu Ser		
370	375	380
Val Cys Pro Leu Asn Ala Lys Val His Tyr Asn Ile Gly Lys Asn Leu		
385	390	395
Ala Asp Lys Gly Asn Gln Thr Ala Ala Ile Arg Tyr Tyr Arg Glu Ala		
405	410	415
Val Arg Leu Asn Pro Lys Tyr Val His Ala Met Asn Asn Leu Gly Asn		
420	425	430
Ile Leu Lys Glu Arg Asn Glu Leu Gln Glu Ala Glu Glu Leu Leu Ser		
435	440	445
Leu Ala Val Gln Ile Gln Pro Asp Phe Ala Ala Ala Trp Met Asn Leu		
450	455	460
Gly Ile Val Gln Asn Ser Leu Lys Arg Phe Glu Ala Ala Glu Gln Ser		
465	470	475
Tyr Arg Thr Ala Ile Lys His Arg Arg Lys Tyr Pro Asp Cys Tyr Tyr		
485	490	495
Asn Leu Gly Arg Leu Tyr Ala Asp Leu Asn Arg His Val Asp Ala Leu		
500	505	510
Asn Ala Trp Arg Asn Ala Thr Val Leu Lys Pro Glu His Ser Leu Ala		
515	520	525

115/233

Trp Asn Asn Met Ile Ile Leu Leu Asp Asn Thr Gly Asn Leu Ala Gln
 530 535 540
 Ala Glu Ala Val Gly Arg Glu Ala Leu Glu Leu Ile Pro Asn Asp His
 545 550 555 560
 Ser Leu Met Phe Ser Leu Ala Asn Val Leu Gly Lys Ser Gln Lys Tyr
 565 570 575
 Lys Glu Ser Glu Ala Leu Phe Leu Lys Ala Ile Lys Ala Asn Pro Asn
 580 585 590
 Ala Ala Ser Tyr His Gly Asn Leu Ala Val Leu Tyr His Arg Trp Gly
 595 600 605
 His Leu Asp Leu Ala Lys Lys His Tyr Glu Ile Ser Leu Gln Leu Asp
 610 615 620
 Pro Thr Ala Ser Gly Thr Lys Glu Asn Tyr Gly Leu Leu Arg Arg Lys
 625 630 635 640
 Leu Glu Leu Met Gln Lys Lys Ala Val
 645

<210> 65

<211> 93

<212> PRT

<213> Homo sapiens

<400> 65

Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro Val Ala
 1 5 10 15
 Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe Tyr
 20 25 30
 Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu Pro
 35 40 45
 Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Ala Ser Leu Leu Ile
 50 55 60
 Val Gly Ala Val Phe Leu Cys Ala Arg Pro Arg Arg Ser Pro Ala Gln
 65 70 75 80
 Glu Asp Gly Lys Val Tyr Ile Asn Met Pro Gly Arg Gly
 85 90

116/233

<210> 66

<211> 425

<212> PRT

<213> Homo sapiens

<400> 66

Met Gly Ser Trp Ala Ala Val Asn Gly Ile Trp Val Glu Leu Pro Val
1 5 10 15
Val Val Lys Glu Leu Pro Glu Gly Trp Ser Leu Pro Ser Tyr Val Ser
20 25 30
Val Leu Val Ala Leu Gly Asn Leu Gly Leu Leu Val Val Thr Leu Trp
35 40 45
Arg Arg Leu Ala Pro Gly Lys Asp Glu Gln Val Pro Ile Arg Val Val
50 55 60
Gln Val Leu Gly Met Val Gly Thr Ala Leu Leu Ala Ser Leu Trp His
65 70 75 80
His Val Ala Pro Val Ala Gly Gln Leu His Ser Val Ala Phe Leu Ala
85 90 95
Leu Ala Phe Val Leu Ala Leu Ala Cys Cys Ala Ser Asn Val Thr Phe
100 105 110
Leu Pro Phe Leu Ser His Leu Pro Pro Arg Phe Leu Arg Ser Phe Phe
115 120 125
Leu Gly Gln Gly Leu Ser Ala Leu Leu Pro Cys Val Leu Ala Leu Val
130 135 140
Gln Gly Val Gly Arg Leu Glu Cys Pro Pro Ala Pro Ile Asn Gly Thr
145 150 155 160
Pro Gly Pro Pro Leu Asp Phe Leu Glu Arg Phe Pro Ala Ser Thr Phe
165 170 175
Phe Trp Ala Leu Thr Ala Leu Leu Val Ala Ser Ala Ala Ala Phe Gln
180 185 190
Gly Leu Leu Leu Leu Leu Pro Pro Pro Pro Ser Val Pro Thr Gly Glu
195 200 205
Leu Gly Ser Gly Leu Gln Val Gly Ala Pro Gly Ala Glu Glu Glu Val
210 215 220
Glu Glu Ser Ser Pro Leu Gln Glu Pro Pro Ser Gln Ala Ala Gly Thr
225 230 235 240

117/233

Thr Pro Gly Pro Asp Pro Lys Ala Tyr Gln Leu Leu Ser Ala Arg Ser
 245 250 255
 Ala Cys Leu Leu Gly Leu Leu Ala Ala Thr Asn Ala Leu Thr Asn Gly
 260 265 270
 Val Leu Pro Ala Val Gln Ser Phe Ser Cys Leu Pro Tyr Gly Arg Leu
 275 280 285
 Ala Tyr His Leu Ala Val Val Leu Gly Ser Ala Ala Asn Pro Leu Ala
 290 295 300
 Cys Phe Leu Ala Met Gly Val Leu Cys Arg Ser Leu Ala Gly Leu Gly
 305 310 315 320
 Gly Leu Ser Leu Leu Gly Val Phe Cys Gly Gly Tyr Leu Met Ala Leu
 325 330 335
 Ala Val Leu Ser Pro Cys Pro Pro Leu Val Gly Thr Ser Ala Gly Val
 340 345 350
 Val Leu Val Val Leu Ser Trp Val Leu Cys Leu Gly Val Phe Ser Tyr
 355 360 365
 Val Lys Val Ala Ala Ser Ser Leu Leu His Gly Gly Gly Arg Pro Ala
 370 375 380
 Leu Leu Ala Ala Gly Val Ala Ile Gln Val Gly Ser Leu Leu Gly Ala
 385 390 395 400
 Val Ala Met Phe Pro Pro Thr Ser Ile Tyr His Val Phe His Ser Arg
 405 410 415
 Lys Asp Cys Ala Asp Pro Cys Asp Ser
 420 425

<210> 67

<211> 149

<212> PRT

<213> Homo sapiens

<400> 67

Met Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn
 1 5 10 15
 Leu Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr
 20 25 30
 Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile

118/233

35 40 45
 Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp
 50 55 60
 Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn
 65 70 75 80
 Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met
 85 90 95
 Gly Gly Leu Gly Phe Ile Ile Leu Asp Arg Ser Asn Ala Pro Asn Ile
 100 105 110
 Pro Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val
 115 120 125
 Leu Leu Ser Phe Phe Met Ala Arg Val Phe Met Arg Met Lys Leu Pro
 130 135 140
 Gly Tyr Leu Met Gly
 145

<210> 68

<211> 396

<212> PRT

<213> Homo sapiens

<400> 68

Met Ala Met Ile Glu Leu Gly Phe Gly Arg Gln Asn Phe His Pro Leu
 1 5 10 15
 Lys Arg Lys Ser Ser Leu Leu Leu Lys Leu Ile Ala Val Val Phe Ala
 20 25 30
 Val Leu Leu Phe Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln
 35 40 45
 Cys Asn Trp Pro Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr
 50 55 60
 Thr Arg Glu Pro Val Leu Lys Ala Met Phe Leu Ala Asp Thr His Leu
 65 70 75 80
 Leu Gly Glu Phe Leu Gly His Trp Leu Asp Lys Leu Arg Arg Glu Trp
 85 90 95
 Gln Met Glu Arg Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu
 100 105 110

119/233

Val Val Phe Ile Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr
 115 120 125
 Pro Glu Ala Trp Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg
 130 135 140
 His Pro Ser His Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile
 145 150 155 160
 Gly Phe His Tyr Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys
 165 170 175
 Val Phe Ser Ser Glu Arg Leu Phe Ser Trp Lys Gly Ile Asn Phe Val
 180 185 190
 Met Val Asn Ser Val Ala Leu Asn Gly Asp Gly Cys Gly Ile Cys Ser
 195 200 205
 Glu Thr Glu Ala Glu Leu Ile Glu Val Ser His Arg Leu Asn Cys Ser
 210 215 220
 Arg Glu Ala Arg Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro
 225 230 235 240
 Thr Ser Ala Pro Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser
 245 250 255
 Asp Ala Asn Cys Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp
 260 265 270
 Ile Pro Phe Lys Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln
 275 280 285
 Lys Leu Leu Trp Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr
 290 295 300
 His Ser Ala Cys Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser
 305 310 315 320
 Val Pro Ser Phe Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met
 325 330 335
 Gly Ser Ile Thr Pro Thr Asp Tyr Thr Leu Ser Lys Cys Tyr Leu Pro
 340 345 350
 Arg Glu Asp Val Val Leu Ile Ile Tyr Cys Gly Val Val Gly Phe Leu
 355 360 365
 Val Val Leu Thr Leu Thr His Phe Gly Leu Leu Ala Ser Pro Phe Leu
 370 375 380
 Ser Gly Leu Asn Leu Leu Gly Lys Arg Lys Thr Arg

120/233

385

390

395

<210> 69

<211> 350

<212> PRT

<213> Homo sapiens

<400> 69

Met Ile Arg Gln Glu Arg Ser Thr Ser Tyr Gln Glu Leu Ser Glu Glu
 1 5 10 15
 Leu Val Gln Val Val Glu Asn Ser Glu Leu Ala Asp Glu Gln Asp Lys
 20 25 30
 Glu Thr Val Arg Val Gln Gly Pro Gly Ile Leu Pro Gly Leu Asp Ser
 35 40 45
 Glu Ser Ala Ser Ser Ser Ile Arg Phe Ser Lys Ala Cys Leu Lys Asn
 50 55 60
 Val Phe Ser Val Leu Leu Ile Phe Ile Tyr Leu Leu Leu Met Ala Val
 65 70 75 80
 Ala Val Phe Leu Val Tyr Arg Thr Ile Thr Asp Phe Arg Glu Lys Leu
 85 90 95
 Lys His Pro Val Met Ser Val Ser Tyr Lys Glu Val Asp Arg Tyr Asp
 100 105 110
 Ala Pro Gly Ile Ala Leu Tyr Pro Gly Gln Ala Gln Leu Leu Ser Cys
 115 120 125
 Lys His His Tyr Glu Val Ile Pro Pro Leu Thr Ser Pro Gly Gln Pro
 130 135 140
 Gly Asp Met Asn Cys Thr Thr Gln Arg Ile Asn Tyr Thr Asp Pro Phe
 145 150 155 160
 Ser Asn Gln Thr Val Lys Ser Ala Leu Ile Val Gln Gly Pro Arg Glu
 165 170 175
 Val Lys Lys Arg Glu Leu Val Phe Leu Gln Phe Arg Leu Asn Lys Ser
 180 185 190
 Ser Glu Asp Phe Ser Ala Ile Asp Tyr Leu Leu Phe Ser Ser Phe Gln
 195 200 205
 Glu Phe Leu Gln Ser Pro Asn Arg Val Gly Phe Met Gln Ala Cys Glu
 210 215 220

121/233

Ser Ala Tyr Ser Ser Trp Lys Phe Ser Gly Gly Phe Arg Thr Trp Val
 225 230 235 240
 Lys Met Ser Leu Val Lys Thr Lys Glu Glu Asp Gly Arg Glu Ala Val
 245 250 255
 Glu Phe Arg Gln Glu Thr Ser Val Val Asn Tyr Ile Asp Gln Arg Pro
 260 265 270
 Ala Ala Lys Lys Ser Ala Gln Leu Phe Phe Val Val Phe Glu Trp Lys
 275 280 285
 Asp Pro Phe Ile Gln Lys Val Gln Asp Ile Val Thr Ala Asn Pro Trp
 290 295 300
 Asn Thr Ile Ala Leu Leu Cys Gly Ala Phe Leu Ala Leu Phe Lys Ala
 305 310 315 320
 Ala Glu Phe Ala Lys Leu Ser Ile Lys Trp Met Ile Lys Ile Arg Lys
 325 330 335
 Arg Tyr Leu Lys Arg Arg Gly Gln Ala Thr Ser His Ile Ser
 340 345 350

<210> 70

<211> 153

<212> PRT

<213> Homo sapiens

<400> 70

Met Thr Ile His Ile Leu Ile Leu Leu Leu Leu Ala Phe Ser Ala
 1 5 10 15
 Gln Gly Asp Leu Asp Thr Ala Ala Arg Arg Gly Gln His Gln Val Pro
 20 25 30
 Gln His Arg Gly His Val Cys Tyr Leu Gly Val Cys Arg Thr His Arg
 35 40 45
 Leu Ala Glu Ile Ile Tyr Trp Ile Arg Cys Leu His Gln Gly Ala Leu
 50 55 60
 Gly Glu Gly Gln Pro Arg Ala Pro Gly Pro Leu Gln Leu Trp Ala Pro
 65 70 75 80
 Pro Val Ala Arg Gly Gly Ser Pro Ala Arg Phe Pro Gly Phe Arg Pro
 85 90 95
 Ala Ala Arg Gly Leu Ala Gln Cys Pro Ala Arg Trp Val Thr Ser Gly

122/233

100 105 110
 Thr Ala Arg Pro Leu Leu Gly Phe Ser Leu Pro Ile Cys Met Leu Glu
 115 120 125
 Leu Leu Leu His Ile Ser Ser Pro Leu Thr Pro Ala Pro Glu Thr Val
 130 135 140
 Phe Pro Ser Pro Ser Pro Gly Cys Asp
 145 150

<210> 71

<211> 1176

<212> DNA

<213> Homo sapiens

<400> 71

atggaggaggag tgagcgcgct gctggcccgc tgccccacgg ccggcctggc cggcggcctg 60
 ggggtcacgg cgtgcgcgcg gcccggcgtg ttgctctacc ggatcgcgcg gaggatgaag 120
 ccaacgcaca cgatggtcaa ctgctgggttc tgcaaccagg atacgtgggt gccctatggg 180
 aaccgcaact gctgggactg tccccactgc gagcagtaca acggettcca ggagaacggc 240
 gactacaaca agccgatccc cgcccagtac ttggagcacc tgaaccacgt ggtgagcagc 300
 gcgcccagcc tgcgcgaccc ttgcgagccg cagcagtggg tgagcagcca agtcctgctg 360
 tgcaagaggt gcaaccacca ccagaccacc aagatcaagc agctggccgc cttcgtcccc 420
 cgcgaggagg gcaggtatga cgaggaggtc gaggtgtacc ggcatcacct ggagcagatg 480
 tacaagctgt gcgggcgtg ccaagcggct gtggagtact acatcaagca ccagaaccgc 540
 cagctgcgcg ccctgttctg cagccaccag ttcaagcgcc gggaggccga ccagaccac 600
 gcacagaact tctcctccgc cgtgaagtc ccggtccagg tcatectgct ccgtgccctc 660
 gccttcctgg cctgcgcctt cctactgacc accgcgctgt atggggccag cggacacttc 720
 gcccagggca ccaactgtgc cctggccctg ccacctgggtg gcaatggctc agccacacct 780
 gacaatggca ccaccctgg ggccgagggc tggcggcagt tgcctggcct actccccgag 840
 cacatggcgg agaagctgtg tgaggcctgg gcctttgggc agagccacca gacgggcgtc 900
 gtggcactgg gcctactcac ctgcctgctg gcaatgctgc tggtggccg catcaggctc 960
 cggaggatcg atgcctctg cacctgctg tgggccctgc tgcctgggct gcacctggct 1020
 gagcagcacc tgcaggccgc ctgcctagc tggttagaca cgctcaagtt cagcaccaca 1080
 tctttgtgct gcctggttgg cttcacggcg gctgtggcca caaggaaggc aacgggcccc 1140
 cggaggttcc ggccccgaag gtcagagaag cagcca 1176

<210> 72

123/233

<211> 1491

<212> DNA

<213> Homo sapiens

<400> 72

atggcgctgt ggcgcggtc cgcgtaacgc ggcttcctgg cgctggccgt gggtgcgtc 60
ttcctgctgg agccagagct gccaggtcg gcgctgcgt ctctctggag ctgctgtgt 120
ctggggcccg cgctgcgc cccgggaccc gtctcccccg agggccggtt ggcggcagcc 180
tgggacgcgc ttatcgtgc gccagtcgg cgctggcgcc gcgtggcagt gggagtcaat 240
gcatgtgttg atgtggtgct ctcaggggtg aagctcttgc aggcacttgg ccttagtcct 300
gggaatggga aagatcacag cattctgcat tcaaggaatg atctggaaga agccttcatt 360
cacttcatgt ggaagggagc agctgctgag cgctcttca gtgataagga aacttttcac 420
gacattgccc aggttgcgtc agagtccca ggagcccagc actatgtagg aggaaatgca 480
gctttaattg gacagaaatt tgcagccaac tcagatttaa aggttcttct ttgcggtcca 540
gttggtccaa ggctacatga gcttcttgat gacaatgtct ttgttccacc agagtcattg 600
caggaagtgg atgagttcca cctcatttta gagtatcaag caggggagga gtggggccag 660
ttaaagctc cccatgcca cggattcatc ttctctcacg acctctcaa cggggccatg 720
aatatgctgg aggtgttgt gtctagcctg gaggagtctc agccagacct ggtggtcctc 780
tctgattgc acatgatgga gggacaaagc aaggagctcc agaggaagag actcttggag 840
gttgtaacct ccatttctga catccccact ggtattccag ttcacctaga gctggccagt 900
atgactaaca gggagctcat ggcagcatt gtccatcagc aggtcttcc cgcggtgact 960
tcccttgggc tgaatgaaca ggagctgtta tttctcacc agtcagctc tggacctcac 1020
tcttctctct ctctctgaa cggtgttct gatgtgggca tggtcagtga catcctcttc 1080
tggatcttga aagaacatgg gaggagtaaa agcagagcct cggatctcac caggatccat 1140
ttcacacgc tggctacca catcctggca actgtggatg gacactgggc caaccagctg 1200
gcagccgtgg ctgcaggagc tcgtgtggtt gggacacagg cctgcgccac agaaaccata 1260
gacaccagcc gagtgtctct gagggcacc caagagtcca tgacttccca ttcggaggca 1320
ggctccagga ttgtattaaa cccaaacaag ccagtagtag aatggcacag agagggata 1380
tccttccact tcacaccagt attggtgtgt aaagaccca ttcgaactgt aggccttggga 1440
gatgccattt cagccgaagg actctctat tcggaagta caccctcacta t 1491

<210> 73

<211> 1251

<212> DNA

<213> Homo sapiens

<400> 73

124/233

atgctggtgc	atttatttcg	ggtcgggatt	cggggtggcc	cattcccagg	caggetgeta	60
ccgcccctcc	gcttccagac	attctcagct	gtcaggtact	ctgatggcta	ccgcagctcc	120
tcctctctcc	gggccttgge	ccacctgcgg	tcccagctct	gggcccacct	ccctcgagcc	180
cccctagctc	ccagatggag	cccctctgcc	tgggtgctggg	ttgggggagc	cctgctaggg	240
cccattggtac	tgagtaagca	tccccacctc	tgccttctgg	ccctgtgtga	ggcagaagag	300
gcccctctcg	ccagctccac	accccatgtc	gtgggggtctc	gctttaactg	gaagctcttc	360
tggcagtttc	tgcaccccca	cctgctgggc	ctgggggtag	ccgtcgtgct	ggccttgggt	420
gcggcactcg	tgaatgtaca	gatccccctg	ctcctgggcc	agctggtaga	ggtcgtggcc	480
aagtacacaa	gggaccacgt	agggagtctc	atgactgagt	cccagaatct	cagcaccac	540
ctgcttatcc	tctatggtgt	ccagggactg	ctgaccttcg	ggtacctggt	gctgctgtcc	600
cacgttggcg	agcgcattgg	tgtggacatg	cggaggggcc	tcttcagctc	cctgctccgg	660
tactgccagc	cgcagggtgc	agagttggga	caagacatca	ccttctttga	cgccaataag	720
acagggcagc	tggtagagcc	cttgacaact	gacgtgcagg	agtttaagtc	atccttcaag	780
cttgtcatct	cccaggggct	gcgaagctgc	accaggtgg	caggctgcct	ggtgtccctg	840
tccatgctgt	cgacacgcct	cacgtctctg	ctgatggtgg	ccacaccagc	cctgatggga	900
gtgggcaccc	tgatgggtcc	aggcctccga	aaattgtctt	gccagtgtca	ggagcagatc	960
gccagggcaa	tgggcgtagc	agacgaggcc	ctgggcaatg	tgcggactgt	gcgtgccttc	1020
gccatggagc	aacgggaaga	ggagcgctat	ggggcagagc	tggaaacctg	ccgctgccgg	1080
gcagaggagc	tgggcgcggg	catcgctctg	ttccaagggc	tttccaacat	cgcttcaac	1140
tgcattggtct	tgggtacctt	atttattggg	ggctcccttg	tggccggaca	gcagctgaca	1200
gggggagacc	tcatgtcctt	cctggtggcc	tcccagacag	tgcaaaggct	g	1251

<210> 74

<211> 1947

<212> DNA

<213> Homo sapiens

<400> 74

atgattccta	accagcataa	tgtcggagcc	gggagccacc	aacctgcagt	tttcagaatg	60
gccgtgttgg	acaactgattt	ggatcacatt	cttccatctt	ctgtttcttc	tccattctgg	120
gctaagttag	tagtgggac	ggttgccatt	gtgtgttttg	cacgcagcta	tgatggagac	180
tttgtctttg	atgactcaga	agctattgtt	aacaataagg	ttgtcgtgtg	tgtcggccgt	240
gcagacctcc	tgtgtgccct	gttcttcttg	ttatctttcc	ttggctactg	taaagcattt	300
agagaaagta	acaaggaggg	agcgcattct	tccaccttct	gggtgctgct	gagtatcttt	360
ctgggagcag	tggccatgct	gtgcaaagag	caagggatca	ctgtgctggg	tttaaatgcg	420
gtatttgaca	tcttggtgat	aggcaaattc	aatgttcttg	aaattgtcca	gaaggacta	480

125/233

cataaggaca agtcattaga gaatctcggc atgctcagga acgggggcct cctcttcaga 540
atgacctgc tcacctctgg aggggctggg atgctctacg tgcgctggag gatcatgggc 600
acggggccgc cgcccttcac cgaggtggac aaccggcct cctttgctga cagcatgctg 660
gtgagggccg taaactacaa ttactactat tcattgaatg cctggctgct gctgtgtccc 720
tggtggctgt gttttgattg gtcaatgggc tgcaccccc tcattaagtc catcagcgac 780
tggagggtaa ttgcaettgc agcactctgg ttctgcctaa ttggcctgat atgccaagcc 840
ctgtgctctg aagacggcca caagagaagg atccttactc tgggcctggg atttctcgtt 900
atcccatctc tccccgcgag taacctgttc ttccgagtgg gcttcgtggt cgcggagcgt 960
gtcctctacc tccccagcat tgggtactgt gtgctgctga cttttggatt cggagccctg 1020
agcaaacata ccaagaaaa gaaactcatt gccgctgtcg tgcagggaat cttattcatc 1080
aacacgctga gatgtgtgct gcgcagcggc gaggggcga gtgaggaaca gcttttcaga 1140
agtgtctgt ctgtgtgtcc cctcaatgct aagggttact acaacattgg caaaaacctg 1200
gctgataaag gcaaccagac agctgccatc agatactacc gggaagctgt aagattaaat 1260
cccaagtatg ttcattgccat gaataatctt ggaaatatct taaaagaaag gaatgagcta 1320
caggaagctg aggagctgct gtctttggct gttcaaatac agccagactt tgccgctgcg 1380
tggtatgaatc taggcatagt gcagaatagc ctgaaacggg ttgaagcagc agagcaaagt 1440
taccggacag caattaaaca cagaaggaaa taccagact gttactacaa cctcgggcgt 1500
ctgtatgcag atctcaatcg ccacgtggat gccttgaatg cgtggagaaa tgccaccgtg 1560
ctgaaaccag agcacagcct ggccctggaac aacatgatta tactcctcga caatacaggt 1620
aatttagccc aagctgaagc agttggaaga gaggcactgg aattaatacc taatgatcac 1680
tctctcatgt tctcgttggc aaacgtgctg gggaaatccc agaaatacaa ggaatctgaa 1740
gctttattcc tcaaggcaat taaagcaaat ccaaatgctg caagttacca tggtaatttg 1800
gctgtgcttt atcatcgttg gggacatcta gacttggcca agaaacacta tgaaatctcc 1860
ttgcagcttg accccacggc atcaggaact aaggagaatt acggtctgct gagaagaaag 1920
ctagaactaa tgcaaaagaa agctgtc 1947

<210> 75

<211> 279

<212> DNA

<213> Homo sapiens

<400> 75

atgatccatc tgggtcacat cctcttcctg cttttgctcc cagtggctgc agctcagacg 60
actccaggag agagatcatc actccctgcc ttttacctg gcacttcagg ctcttgttcc 120
ggatgtgggt ccctctctct gccgctcctg gcaggcctcg tggctgctga tgcggtggca 180
tcgctgctca tcgtgggggc ggtgttctg tgcgcacgcc cacgcgcag ccccgcccaa 240

126/233

gaagatggca aagtctacat caacatgccca ggcaggggc

279

<210> 76

<211> 1275

<212> DNA

<213> Homo sapiens

<400> 76

atgggctcct gggetgoggt caatgggac	tgggtggagc tacctgtggt ggtcaaagag	60
cttccagagg gttggagcct cccctcttac	gtctctgtgc ttgtggctct ggggaacctg	120
gggtctgctgg tggtagccct ctggaggagg	ctggccccag gaaaggacga gcaggtcccc	180
atccgggtgg tgcaggtgct gggcatggtg	ggcacagccc tgetggcctc tctgtggcac	240
catgtggccc cagtggcagg acagttgcat	tctgtggcct tcttagcaact ggcctttgtg	300
ctggcactgg catgctgtgc ctgaatgtc	actttcctgc ccttcttgag ccacctgcc	360
cctcgcttct tacggtcatt cttcctgggt	caaggcctga gtgccctgct gccctgctg	420
ctggccctag tgcaggggtg gggccgctc	gagtggccgc cagcccccat caacggcacc	480
cctggccccc cgtctgactt ccttgagcgt	tttcccgcca gcaccttctt ctgggcactg	540
actgcccttc tggtegettc agctgtgcc	ttccagggtc ttctgctgct gttgccgcca	600
ccaccatctg taccacacagg ggagttagga	tcaggcctcc aggtgggagc cccaggagca	660
gaggaagagg tgggaagagtc ctcaccactg	caagagccac caagccaggc agcaggcacc	720
acccttggtc cagaccctaa ggcctatcag	cttctatcag cccgcagtgc ctgcctgctg	780
ggcctgttg cgcacaccaa cgcgctgacc	aatggcgtgc tgcctgccgt gcagagcttt	840
tcctgettac cctacgggag tctggcctac	cacctggctg tgggtgctggg cagtgtgcc	900
aatccctgg cctgcttcct ggccatgggt	gtgctgtgca ggtccttggc agggctgggc	960
ggcctctctc tgetgggct gttctgtggg	ggctacctga tggcgctggc agtcctgagc	1020
ccctgcccgc cctgggtggg cacctcgagg	gggggtggcc tegtgggtgct gtcgtgggtg	1080
ctgtgtcttg gcgtgttctc ctacgtgaag	gtggcagcca gctccctgct gcatggcggg	1140
ggccggccgg cattgctggc agccggcgtg	gccatccagg tgggctctct gtcggcgct	1200
gttgctatgt tcccccgac cagcatctat	cacgtgttcc acagcagaaa ggactgtgca	1260
gaccctgtg actcc		1275

<210> 77

<211> 447

<212> DNA

<213> Homo sapiens

<400> 77

127/233

atggagactt tgtaccgtgt cccgttctta gtgctcgaat gtcccaacct gaagctgaag	60
aagccgccct ggttgccat gccgtcgcc atgactgtgt atgctctggt ggtggtgtct	120
tacttctca tcaccggagg aataatttat gatgttattg ttgaacctcc aagtgtcggt	180
tctatgactg atgaacatgg gcacagagg ccagtagctt tcttgcccta cagagtaaat	240
ggacaatata ttatggaagg acttgcatcc agcttctat ttacaatggg aggtttaggt	300
ttcataatcc tggaccgac gaatgcacca aatatcccaa aactcaatag attccttctt	360
ctgttcattg gattcgtctg tgctctattg agttttttca tggctagagt attcatgaga	420
atgaaactgc cgggctatct gatgggt	447

<210> 78

<211> 1188

<212> DNA

<213> Homo sapiens

<400> 78

atggcgatga tgaattggg gtttgaaga cagaattttc atccattaaa gaggaagagt	60
tcattgctgt tgaactcat agctgtgtc tttgctgtc ttctattttg tgaattttta	120
atctattact tagcgatctt tcagtgtaat tggcctgaag tgaaaaccac agcctctgat	180
ggtgaacaga ccacacgtga gcctgtgtc aaagccatgt ttttggtga caccctttg	240
cttggggaat tcctaggcca ctggctggac aaattacgaa gggaatggca gatggagaga	300
ggttccaga cagctctgtg gttgctgcag ccggaagtcg tottcatcct gggggatata	360
tttgatgaag ggaagtggag caccctgag gcctggcgagg atgatgtgga gcggtttcag	420
aaaatgttca gacaccaag tcatgtacag ctgaaggtag ttgctggaaa ccatgacatt	480
ggcttccatt atgagatgaa cacatacaaa gtagaacgct ttgagaaagt gttcagctct	540
gaaagactgt tttcttggaa aggcattaac tttgtgatgg tcaacagcgt ggcgtgaac	600
ggggatggct gtggcatctg ctctgaaaca gaagcagagc tcattgaagt ttctcacaga	660
ctgaactgct ccgagaggc acgtggctcc agccggtgtg gacctgggcc totgtgccc	720
acgtctgccc ctgtctctc gcagcattat cctctgtatc ggagaagtga tgctaactgt	780
tctggggaag acgtgtctc tgcagaggaa agggacatcc catttaagga gaactatgac	840
gtgctttcac gggaggcatc acaaaagctg ctgtggtggc tccagccgcg cctggttctc	900
agtggccaca cgcacagcgc ctgagagggt caccacgggg gccgagtccc cgagctcagc	960
gtcccatctt tcagttggag gaacagaaac aacccagtt tcatcatggg tagcatcacg	1020
cccacagact acaccctctc caagtgtctc ctcccacgtg aggatgtggt tttgatcctc	1080
tactgtggag tgggtgggct ccttgtggtc ctccactca ctacttttg gcttctagcc	1140
tcaccttttc tttctggttt gaacttgctc ggaaagcgta agacaaga	1188

128/233

<210> 79

<211> 1050

<212> DNA

<213> Homo sapiens

<400> 79

atgatccggc	aggagcgctc	cacatcctac	caggagctga	gtgaggagt	gggccagggtg	60
gttgagaact	cagagctggc	agacgagcag	gacaaggaga	cggtcagagt	ccaagggtccg	120
ggtatcttac	caggcctgga	cagcgagtcc	gcctccagca	gcacccgctt	cagcaaggcc	180
tgcctgaaga	acgtcttctc	ggtcctactc	atcttcatct	acctgctgct	catggctgtg	240
gccgtcttcc	tgggtctaccg	gaccatcaca	gactttcggtg	agaaactcaa	gcacctgtc	300
atgtctgtgt	cttacaagga	agtggatcgc	tatgatgccc	caggatttgc	cttgtacccc	360
ggtcaggccc	agttgctcag	ctgtaagcac	cattacgagg	tcattcctcc	tctgacaagc	420
cctggccagc	cgggtgacat	gaattgcacc	acccagagga	tcaactacac	ggaccccttc	480
tccaatcaga	ctgtgaaatc	tgccctgatt	gtccaggggc	cccgggaagt	gaaaaagcgg	540
gagctggtct	tcctccagtt	ccgcctgaac	aagagtagtg	aggacttcag	cgccattgat	600
tacctcctct	tctcttcttt	ccaggagttc	ctgcaaagcc	caaacagggt	aggcttcatg	660
caggcctgtg	agagtgccta	ttccagctgg	aagttctctg	ggggcttccg	cacctgggtc	720
aagatgtcac	tggtaaagac	caaggaggag	gatgggcggg	aagcagtgga	gttccggcag	780
gagacaagtg	tggttaaacta	cattgaccag	aggccagctg	ccaaaaaag	tgctcaattg	840
ttttttgtgg	tctttgaatg	gaaagatcct	ttcatccaga	aagtccaaga	tatagtcact	900
gccaatcctt	ggaacacaat	tgctcttctc	tgtggcgccct	tcttggcatt	atttaaagca	960
gcagagtttg	ccaaactgag	tataaaatgg	atgatcaaaa	ttagaaagag	ataccttaaa	1020
agaagaggtc	aggcaacgag	ccacataagc				1050

<210> 80

<211> 459

<212> DNA

<213> Homo sapiens

<400> 80

atgactatcc	acatcctcat	cctgctgttg	ctcctcgccct	tctccgccca	aggggacctg	60
gacactgcag	ccaggcgagg	ccagcaccag	gtcccccagc	accgcgggca	cgtctgctac	120
ctgggcgtat	gccggaccca	ccgcctggcg	gagatcatat	actggattcg	ctgtctccac	180
caaggagccc	tccgggaagg	ccagccacga	gccccaggac	ccctacagct	atgggcgccg	240
ccggtggcgc	gaggcggaag	cccggctcgg	ttcccaggat	tccggcctgc	agcgaggggg	300
ctagcgcagt	gcccagctcg	ctgggtgacc	tccggcacgg	ctcgccccct	cctcggtctc	360

129/233

agtttgcta tctgtatgtt ggagcttcta ctccacattt cttctccct aactccagcc 420
cctgaaaccg tcttccccag tccctccccg ggetgcgac 459

<210> 81

<211> 4027

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (192)...(1370)

<400> 81

gcccgtaca aagcggcgaa ggtcacggcg cgaggaggcg cgcgtcgccg ccccgcgtaa 60
cgctgcggc ccgcgcccc ggctgcaccg cctcctgcc gcctgcccgc ctgcccgcct 120
gcccgcctac ccgcctacc gcctaccgc ctacccccct gccggcctgc cgtccttcca 180
cgcgagagagc c atg gag gga gtg agc gcg ctg ctg gcc cgc tgc ccc acg 230
Met Glu Gly Val Ser Ala Leu Leu Ala Arg Cys Pro Thr
1 5 10
gcc gcc ctg gcc gcc gcc ctg ggg gtc acg gcg tgc gcc gcg gcc gcc 278
Ala Gly Leu Ala Gly Gly Leu Gly Val Thr Ala Cys Ala Ala Ala Gly
15 20 25
gtg ttg ctc tac cgg atc gcg cgg agg atg aag cca acg cac acg atg 326
Val Leu Leu Tyr Arg Ile Ala Arg Arg Met Lys Pro Thr His Thr Met
30 35 40 45
gtc aac tgc tgg ttc tgc aac cag gat acg ctg gtg ccc tat ggg aac 374
Val Asn Cys Trp Phe Cys Asn Gln Asp Thr Leu Val Pro Tyr Gly Asn
50 55 60
cgc aac tgc tgg gac tgt ccc cac tgc gag cag tac aac gcc ttc cag 422
Arg Asn Cys Trp Asp Cys Pro His Cys Glu Gln Tyr Asn Gly Phe Gln
65 70 75
gag aac gcc gac tac aac aag ccg atc ccc gcc cag tac ttg gag cac 470
Glu Asn Gly Asp Tyr Asn Lys Pro Ile Pro Ala Gln Tyr Leu Glu His
80 85 90
ctg aac cac gtg gtg agc agc gcg ccc agc ctg cgc gac cct tcg cag 518
Leu Asn His Val Val Ser Ser Ala Pro Ser Leu Arg Asp Pro Ser Gln
95 100 105

130/233

ccg cag cag tgg gtg agc agc caa gtc ctg ctg tgc aag agg tgc aac	566
Pro Gln Gln Trp Val Ser Ser Gln Val Leu Leu Cys Lys Arg Cys Asn	
110 115 120 125	
cac cac cag acc acc aag atc aag cag ctg gcc gcc ttc gct ccc cgc	614
His His Gln Thr Thr Lys Ile Lys Gln Leu Ala Ala Phe Ala Pro Arg	
130 135 140	
gag gag ggc agg tat gac gag gag gtc gag gtg tac cgg cat cac ctg	662
Glu Glu Gly Arg Tyr Asp Glu Glu Val Glu Val Tyr Arg His His Leu	
145 150 155	
gag cag atg tac aag ctg tgc cgg ccg tgc caa gcg gct gtg gag tac	710
Glu Gln Met Tyr Lys Leu Cys Arg Pro Cys Gln Ala Ala Val Glu Tyr	
160 165 170	
tac atc aag cac cag aac cgc cag ctg cgc gcc ctg ttg ctc agc cac	758
Tyr Ile Lys His Gln Asn Arg Gln Leu Arg Ala Leu Leu Leu Ser His	
175 180 185	
cag ttc aag cgc cgg gag gcc gac cag acc cac gca cag aac ttc tcc	806
Gln Phe Lys Arg Arg Glu Ala Asp Gln Thr His Ala Gln Asn Phe Ser	
190 195 200 205	
tcc gcc gtg aag tcc ccg gtc cag gtc atc ctg ctc cgt gcc ctc gcc	854
Ser Ala Val Lys Ser Pro Val Gln Val Ile Leu Leu Arg Ala Leu Ala	
210 215 220	
ttc ctg gcc tgc gcc ttc cta ctg acc acc gcg ctg tat ggg gcc agc	902
Phe Leu Ala Cys Ala Phe Leu Leu Thr Thr Ala Leu Tyr Gly Ala Ser	
225 230 235	
gga cac ttc gcc cca ggc acc act gtg ccc ctg gcc ctg cca cct ggt	950
Gly His Phe Ala Pro Gly Thr Thr Val Pro Leu Ala Leu Pro Pro Gly	
240 245 250	
ggc aat ggc tca gcc aca cct gac aat ggc acc acc cct ggg gcc gag	998
Gly Asn Gly Ser Ala Thr Pro Asp Asn Gly Thr Thr Pro Gly Ala Glu	
255 260 265	
ggc tgg cgg cag ttg ctg ggc cta ctc ccc gag cac atg gcg gag aag	1046
Gly Trp Arg Gln Leu Leu Gly Leu Leu Pro Glu His Met Ala Glu Lys	
270 275 280 285	
ctg tgt gag gcc tgg gcc ttt ggg cag agc cac cag acg ggc gtc gtg	1094
Leu Cys Glu Ala Trp Ala Phe Gly Gln Ser His Gln Thr Gly Val Val	

131/233

290	295	300	
gca ctg ggc cta ctc acc tgc ctg ctg gca atg ctg ctg gct ggc cgc			1142
Ala Leu Gly Leu Leu Thr Cys Leu Leu Ala Met Leu Leu Ala Gly Arg			
305	310	315	
atc agg ctc cgg agg atc gat gcc ttc tgc acc tgc ctg tgg gcc ctg			1190
Ile Arg Leu Arg Arg Ile Asp Ala Phe Cys Thr Cys Leu Trp Ala Leu			
320	325	330	
ctg ctg ggg ctg cac ctg gct gag cag cac ctg cag gcc gcc tcg cct			1238
Leu Leu Gly Leu His Leu Ala Glu Gln His Leu Gln Ala Ala Ser Pro			
335	340	345	
agc tgg cta gac acg ctc aag ttc agc acc aca tct ttg tgc tgc ctg			1286
Ser Trp Leu Asp Thr Leu Lys Phe Ser Thr Thr Ser Leu Cys Cys Leu			
350	355	360	365
gtt ggc ttc acg gcg gct gtg gcc aca agg aag gca acg ggc cca cgg			1334
Val Gly Phe Thr Ala Ala Val Ala Thr Arg Lys Ala Thr Gly Pro Arg			
370	375	380	
agg ttc cgg ccc cga agg tca gag aag cag cca tgactgcggg ggg			1380
Arg Phe Arg Pro Arg Arg Ser Glu Lys Gln Pro			
385	390		
aggacacacg gatgctcagg cccaggcttt gccagggtccg aagcggggccc ctctctgtcc			1440
tgcctctttt cacctgctca cgccctccca cccccaccct acageccccag gtccctggccc			1500
agtcctccca ctgcctcgaa gagtcagtct gccctgcctt ttcttttcgg gcaccaccag			1560
ccatccccga gtgccctgta gccactcacc actgctgcca cctctctggc caatggccct			1620
ttcactggcc tggtgactgg aatgtgggca gcgcccacac aggtctctggc ccatggcttc			1680
ctactggcag ctccaggcac cccccctctca ccacgcctt tgetggctct gacactgttg			1740
ggtgagggtc ctggtcctgc tgtcttccct tctggcctct gcacaggggt ggtgacagtg			1800
gctacaggct gggccctgg cgtgccctga cctgcagca gagtgaggct ggggcagcag			1860
agagccccag cctcaccct gaggagcacc tgtgggtctgt ccccttggtc ctgcttatgg			1920
ctggaccggc cctgcaggag gtggtggagc cgtgaaggag gccgagctgc agctctggct			1980
gctgcttggc ctctgctcc aagaccctcc cgagtccccg gaaatggaga gtgcagttct			2040
tgggcccagc ctggccttcg ccatgagttt ggggagcgag accccacctg agacaggcag			2100
taggagcctg tgctgacctt ggggaatctg agcttttcca agggtaaggg gcccagggtg			2160
tgcaggcctt cagtgcacac aggtcgttgt cctctttcc ctccctgacc tgtcacgagc			2220
ctctgcagggt gcctgctcac catggcccag cgccactctg tctccgact cagggtgagg			2280
ggcagcccac agacctgctc ctccagtagca gggcctggcc aggccctgc tgttctcagc			2340

132/233

```

ctcagtttgc catctatgaa atgaggtgga cccctctcca tagcccttgg gtgccagetc 2400
agtgggtgtg gggatcacat gaggtggctc atgaggacac actctggaag tcgaggggct 2460
gccacgtgca gaggaagtcc cgggcctggg ggctttatcc aggggtccca gtcgagagtg 2520
gcccagaggcc gtccctcacc gggcatgttc cctctggctg cccactccct cagggccccc 2580
atgtcctgcc actcgccact ctgagcacga gttcaccttc cagatgtggc caggggtgtgc 2640
cagtcctctc ctctgtgctg ttggaacccc gggggaggga agagcagatc acaggtgcat 2700
gaggggttaca cccgtcacct gggctctgcc ggatgggttg ggggggcagg tgccaggcct 2760
cactgctgtg aatctgccac gcctgggggt cctagagggt gccccacccc agtgattggg 2820
tagcagetc aatccccccc agcttcacaa gtgaggaacc caggtgcacg gggagaccct 2880
cgggggcttc tgtggcctct gtgccgatg acctgcgtgg ctccagacaa gggcccgagc 2940
ttactgggct cagcttggtg ttctgtgtgg agcgtgaggt gagaaaaccc ctctgaaaag 3000
atgtggctcg ggcacgctt cccactgggt ctgcagttag gagggtgggc gggtagacca 3060
aagcggcccc ccattggtgc tacctgaggg gcagggaacc gcctgcctgt gcactcacgc 3120
cacccccag cccacaaaga gccatctga gagaaggacg tggtagagcc aggacgggaa 3180
agcgtcctgt cggctggcca tgctgttget tgcgtctcga atcttcggtt ctcgaggaag 3240
tgttgacagt gtgatgctaa tgcctgcttt tcttgccgtt gggtagaagc aggacatctg 3300
tgtgtatgtg cgtattttaa ttagattatt tataataacc agagccagcc ctccgctgtg 3360
ccaggatcct cctgccgagc tgatgtcgtc cctgccctct gccgggggtc ggaagcgaca 3420
tctcaggagg tagctctcag cagagttagg attcctgcct ttcgtagagt tttgtgtgac 3480
tttttaaaatt attcatgtgt cccttaaaag tttcactacg tggagaaaat tccagacca 3540
agtgttgtgg caacagctga gagagtgcag gcaccactgt gttgtggctt gttgaccggg 3600
aatgtgtcac ccctgccagg gaactctctc cctcgcgggg gacttgggat ggccatcaga 3660
cctctagagg tctggctggg gtaatcctag gtatgggtga ccgtccctga gacataagcg 3720
aggtagatcc agccatctc accctcagac ttgaggtecc caccagggcc aagccggccc 3780
cccgtacccc ttgcctggga gcaaaccgcc aggacgcagc ctccacgccg cacctgccac 3840
accagccct gccaggaag gaacacatga ccctctgtc tgtgactgtt gctgagtctc 3900
tgtctcatgt cgtagaattg tggataattg tctagtacc ctctcatcac tgtaaccatc 3960
gcgcctggcc tagatgtcgt gttttggatg ctgtgttttc aataaatgcc tctggggccc 4020
tgctttt 4027

```

<210> 82

<211> 2495

<212> DNA

<213> Homo sapiens

<220>

133/233

<221> CDS

<222> (30)...(1523)

<400> 82

```

gttcgcgcag gtggggcgcc tgggtcccc atg gcg ctg tgg cgc ggc tcc gcg      53
                               Met Ala Leu Trp Arg Gly Ser Ala
                               1           5

tac gcg ggc ttc ctg gcg ctg gcc gtg ggc tgc gtc ttc ctg ctg gag      101
Tyr Ala Gly Phe Leu Ala Leu Ala Val Gly Cys Val Phe Leu Leu Glu
      10           15           20

cca gag ctg cca ggc tcg gcg ctg cgc tct ctc tgg agc tcg ctg tgt      149
Pro Glu Leu Pro Gly Ser Ala Leu Arg Ser Leu Trp Ser Ser Leu Cys
      25           30           35           40

ctg ggg ccc gcg cct gcg ccc ccg gga ccc gtc tcc ccc gag ggc cgg      197
Leu Gly Pro Ala Pro Ala Pro Pro Gly Pro Val Ser Pro Glu Gly Arg
              45           50           55

ttg gcg gca gcc tgg gac gcg ctt atc gtg cgg cca gtc cgg cgc tgg      245
Leu Ala Ala Ala Trp Asp Ala Leu Ile Val Arg Pro Val Arg Arg Trp
              60           65           70

cgc cgc gtg gca gtg gga gtc aat gca tgt gtt gat gtg gtg ctc tca      293
Arg Arg Val Ala Val Gly Val Asn Ala Cys Val Asp Val Val Leu Ser
              75           80           85

ggg gtg aag ctc ttg cag gca ctt ggc ctt agt cct ggg aat ggg aaa      341
Gly Val Lys Leu Leu Gln Ala Leu Gly Leu Ser Pro Gly Asn Gly Lys
      90           95           100

gat cac agc att ctg cat tca agg aat gat ctg gaa gaa gcc ttc att      389
Asp His Ser Ile Leu His Ser Arg Asn Asp Leu Glu Glu Ala Phe Ile
      105           110           115           120

cac ttc atg tgg aag gga gca gct gct gag cgc ttc ttc agt gat aag      437
His Phe Met Trp Lys Gly Ala Ala Ala Glu Arg Phe Phe Ser Asp Lys
              125           130           135

gaa act ttt cac gac att gcc cag gtt gcg tca gag ttc cca gga gcc      485
Glu Thr Phe His Asp Ile Ala Gln Val Ala Ser Glu Phe Pro Gly Ala
              140           145           150

cag cac tat gta gga gga aat gca gct tta att gga cag aaa ttt gca      533
Gln His Tyr Val Gly Gly Asn Ala Ala Leu Ile Gly Gln Lys Phe Ala

```

134/233

155	160	165	
gcc aac tca gat tta aag gtt ctt ctt tgc ggt cca gtt ggc cca agg			581
Ala Asn Ser Asp Leu Lys Val Leu Leu Cys Gly Pro Val Gly Pro Arg			
170	175	180	
cta cat gag ctt ctt gat gac aat gtc ttt gtt cca cca gag tca ttg			629
Leu His Glu Leu Leu Asp Asp Asn Val Phe Val Pro Pro Glu Ser Leu			
185	190	195	200
cag gaa gtg gat gag ttc cac ctc att tta gag tat caa gca ggg gag			677
Gln Glu Val Asp Glu Phe His Leu Ile Leu Glu Tyr Gln Ala Gly Glu			
205	210	215	
gag tgg ggc cag tta aaa got ccc cat gcc aac cga ttc atc ttc tct			725
Glu Trp Gly Gln Leu Lys Ala Pro His Ala Asn Arg Phe Ile Phe Ser			
220	225	230	
cac gac ctc tcc aac ggg gcc atg aat atg ctg gag gtg ttt gtg tct			773
His Asp Leu Ser Asn Gly Ala Met Asn Met Leu Glu Val Phe Val Ser			
235	240	245	
agc ctg gag gag ttt cag cca gac ctg gtg gtc ctc tct gga ttg cac			821
Ser Leu Glu Glu Phe Gln Pro Asp Leu Val Val Leu Ser Gly Leu His			
250	255	260	
atg atg gag gga caa agc aag gag ctc cag agg aag aga ctc ttg gag			869
Met Met Glu Gly Gln Ser Lys Glu Leu Gln Arg Lys Arg Leu Leu Glu			
265	270	275	280
gtt gta acc tcc att tct gac atc ccc act ggt att cca gtt cac cta			917
Val Val Thr Ser Ile Ser Asp Ile Pro Thr Gly Ile Pro Val His Leu			
285	290	295	
gag ctg gcc agt atg act aac agg gag ctc atg agc agc att gtc cat			965
Glu Leu Ala Ser Met Thr Asn Arg Glu Leu Met Ser Ser Ile Val His			
300	305	310	
cag cag gtc ttt ccc gcg gtg act tcc ctt ggg ctg aat gaa cag gag			1013
Gln Gln Val Phe Pro Ala Val Thr Ser Leu Gly Leu Asn Glu Gln Glu			
315	320	325	
ctg tta ttt ctc acc cag tca gcc tct gga cct cac tct tct ctc tct			1061
Leu Leu Phe Leu Thr Gln Ser Ala Ser Gly Pro His Ser Ser Leu Ser			
330	335	340	
tcc tgg aac ggt gtt cct gat gtg ggc atg gtc agt gac atc ctc ttc			1109

135/233

Ser Trp Asn Gly Val Pro Asp Val Gly Met Val Ser Asp Ile Leu Phe
 345 350 355 360
 tgg atc ttg aaa gaa cat ggg agg agt aaa agc aga gcc tog gat ctc 1157
 Trp Ile Leu Lys Glu His Gly Arg Ser Lys Ser Arg Ala Ser Asp Leu
 365 370 375
 acc agg atc cat ttc cac acg ctg gtc tac cac atc ctg gca act gtg 1205
 Thr Arg Ile His Phe His Thr Leu Val Tyr His Ile Leu Ala Thr Val
 380 385 390
 gat gga cac tgg gcc aac cag ctg gca gcc gtg gct gca gga gct cgt 1253
 Asp Gly His Trp Ala Asn Gln Leu Ala Ala Val Ala Ala Gly Ala Arg
 395 400 405
 gtg gct ggg aca cag gcc tgc gcc aca gaa acc ata gac acc agc cga 1301
 Val Ala Gly Thr Gln Ala Cys Ala Thr Glu Thr Ile Asp Thr Ser Arg
 410 415 420
 gtg tct ctg agg gca ccc caa gag ttc atg act tcc cat tcg gag gca 1349
 Val Ser Leu Arg Ala Pro Gln Glu Phe Met Thr Ser His Ser Glu Ala
 425 430 435 440
 ggc tcc agg att gta tta aac cca aac aag cca gta gta gaa tgg cac 1397
 Gly Ser Arg Ile Val Leu Asn Pro Asn Lys Pro Val Val Glu Trp His
 445 450 455
 aga gag gga ata tcc ttc cac ttc aca cca gta ttg gtg tgt aaa gac 1445
 Arg Glu Gly Ile Ser Phe His Phe Thr Pro Val Leu Val Cys Lys Asp
 460 465 470
 ccc att cga act gta ggc ctt gga gat gcc att tca gcc gaa gga ctc 1493
 Pro Ile Arg Thr Val Gly Leu Gly Asp Ala Ile Ser Ala Glu Gly Leu
 475 480 485
 ttc tat tcg gaa gta cac cct cac tat taggaagatt cttaggggta 1540
 Phe Tyr Ser Glu Val His Pro His Tyr
 490 495
 atttttctga ggaaggagaa ctagccaact taagaattac aggaagaaag tggtttggaa 1600
 gacagccaaa gaaataaaaag cagattaaac tgtatcagggt acattccagc ctgttggcaa 1660
 ctcataaaaa acatttcaga ttttaaatcog aatttagcta atgagactgg atttttgttt 1720
 tttatgttgt gtgtcacaga gctaaaaact cagttcccaa atccccagtt tatgcagcgc 1780
 catcagggtat ttttaagctaa acttcttcac ccctgagagc atgtcagctg gagaaaagca 1840
 gttcttcctt gcccaactga gaagtgcacg cccactcacc caacatcctg gtctctagga 1900

136/233

aagcctcatg tgaggttccct ctttctttca gctcagtgcc catgggcaag gatcatgatt 1960
tccattccgt gttacaatga caatatttaa tgagcataac cttctcagtc tccgtctctc 2020
aaatttagga cagagccgct aaggacaaaa caatccctcc cgtgctttat gatggcagca 2080
ggggctgggg agcctctgag ggactctttc attctgcagt tgtctggaag cctgggtggc 2140
gtcatgagct gaaggatcat gctttcctgt cctggctcca taggttatag gctggctggt 2200
gaaaggttca cgtggcccag gctgaacttc attgcctagc tttggatgtg ctttctgcca 2260
taaagactga tttttgttcg ttctgagcct tcaaggaatt tgttttttac aactggaata 2320
tgctcctgtg tgtgttaaca gatcatggat gttttatgtt ttcactgac atttaaagag 2380
tttgacctca gagctccagg atcatcagta aatttgteat gttatatatt tattttttta 2440
taaatcaaga cttctgtgtg ctcttaaata tattaaaaac aatttacatt tcagg 2495

<210> 83

<211> 1617

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (67)...(1320)

<400> 83

atagagccct cagtgggatg aggggtgaaac tgctattgcc ggcggtccct gttttaccgc 60
gtcagc atg ctg gtg cat tta ttt cgg gtc ggg att cgg ggt ggc cca 108
Met Leu Val His Leu Phe Arg Val Gly Ile Arg Gly Gly Pro
1 5 10
ttc cca ggc agg ctg cta ccg ccc ctc cgc ttc cag aca ttc tca gct 156
Phe Pro Gly Arg Leu Leu Pro Pro Leu Arg Phe Gln Thr Phe Ser Ala
15 20 25 30
gtc agg tac tct gat ggc tac cgc agc tcc tcc ctc ctc cgg gcc gtg 204
Val Arg Tyr Ser Asp Gly Tyr Arg Ser Ser Ser Leu Leu Arg Ala Val
35 40 45
gcc cac ctg cgg tcc cag ctc tgg gcc cac ctc cct cga gcc ccc cta 252
Ala His Leu Arg Ser Gln Leu Trp Ala His Leu Pro Arg Ala Pro Leu
50 55 60
gct ccc aga tgg agc ccc tct gcc tgg tgc tgg gtt ggg gga gcc ctg 300
Ala Pro Arg Trp Ser Pro Ser Ala Trp Cys Trp Val Gly Gly Ala Leu
65 70 75

137/233

cta ggc ccc atg gta ctg agt aag cat ccc cac ctc tgc ctt gtg gcc	348
Leu Gly Pro Met Val Leu Ser Lys His Pro His Leu Cys Leu Val Ala	
80 85 90	
ctg tgt gag gca gaa gag gcc cct cct gcc agc tcc aca ccc cat gtc	396
Leu Cys Glu Ala Glu Glu Ala Pro Pro Ala Ser Ser Thr Pro His Val	
95 100 105 110	
gtg ggg tct cgc ttt aac tgg aag ctc ttc tgg cag ttt ctg cac ccc	444
Val Gly Ser Arg Phe Asn Trp Lys Leu Phe Trp Gln Phe Leu His Pro	
115 120 125	
cac ctg ctg gtc ctg ggg gta gcc gtc gtg ctg gcc ttg ggt gcg gca	492
His Leu Leu Val Leu Gly Val Ala Val Val Leu Ala Leu Gly Ala Ala	
130 135 140	
ctc gtg aat gta cag atc ccc ctg ctc ctg ggc cag ctg gta gag gtc	540
Leu Val Asn Val Gln Ile Pro Leu Leu Leu Gly Gln Leu Val Glu Val	
145 150 155	
gtg gcc aag tac aca agg gac cac gta ggg agt ttc atg act gag tcc	588
Val Ala Lys Tyr Thr Arg Asp His Val Gly Ser Phe Met Thr Glu Ser	
160 165 170	
cag aat ctc agc acc cac ctg ctt atc ctc tat ggt gtc cag gga ctg	636
Gln Asn Leu Ser Thr His Leu Leu Ile Leu Tyr Gly Val Gln Gly Leu	
175 180 185 190	
ctg acc ttc ggg tac ctg gtg ctg ctg tcc cac gtt ggc gag cgc atg	684
Leu Thr Phe Gly Tyr Leu Val Leu Leu Ser His Val Gly Glu Arg Met	
195 200 205	
gct gtg gac atg cgg agg gcc ctc ttc agc tcc ctg ctc cgg tac tgc	732
Ala Val Asp Met Arg Arg Ala Leu Phe Ser Ser Leu Leu Arg Tyr Cys	
210 215 220	
cag ccg cag ggt gca gag ttg gga caa gac atc acc ttc ttt gac gcc	780
Gln Pro Gln Gly Ala Glu Leu Gly Gln Asp Ile Thr Phe Phe Asp Ala	
225 230 235	
aat aag aca ggg cag ctg gtg agc cgc ttg aca act gac gtg cag gag	828
Asn Lys Thr Gly Gln Leu Val Ser Arg Leu Thr Thr Asp Val Gln Glu	
240 245 250	
ttt aag tca tcc ttc aag ctt gtc atc tcc cag ggg ctg cga agc tgc	876
Phe Lys Ser Ser Phe Lys Leu Val Ile Ser Gln Gly Leu Arg Ser Cys	

138/233

255	260	265	270	
acc cag gtg gca ggc tgc ctg gtg tcc ctg tcc atg ctg tcg aca cgc				924
Thr Gln Val Ala Gly Cys Leu Val Ser Leu Ser Met Leu Ser Thr Arg				
275	280	285		
ctc acg ctg ctg ctg atg gtg gcc aca cca gcc ctg atg gga gtg ggc				972
Leu Thr Leu Leu Leu Met Val Ala Thr Pro Ala Leu Met Gly Val Gly				
290	295	300		
acc ctg atg ggc tca ggc ctc cga aaa ttg tct tgc cag tgt cag gag				1020
Thr Leu Met Gly Ser Gly Leu Arg Lys Leu Ser Cys Gln Cys Gln Glu				
305	310	315		
cag atc gcc agg gca atg ggc gta gca gac gag gcc ctg ggc aat gtg				1068
Gln Ile Ala Arg Ala Met Gly Val Ala Asp Glu Ala Leu Gly Asn Val				
320	325	330		
cgg act gtg cgt gcc ttc gcc atg gag caa cgg gaa gag gag cgc tat				1116
Arg Thr Val Arg Ala Phe Ala Met Glu Gln Arg Glu Glu Glu Arg Tyr				
335	340	345	350	
ggg gca gag ctg gaa gcc tgc cgc tgc cgg gca gag gag ctg ggc cgc				1164
Gly Ala Glu Leu Glu Ala Cys Arg Cys Arg Ala Glu Glu Leu Gly Arg				
355	360	365		
ggc atc gcc ttg ttc caa ggg ctt tcc aac atc gcc ttc aac tgc atg				1212
Gly Ile Ala Leu Phe Gln Gly Leu Ser Asn Ile Ala Phe Asn Cys Met				
370	375	380		
gtc ttg ggt acc cta ttt att ggg ggc tcc ctt gtg gcc gga cag cag				1260
Val Leu Gly Thr Leu Phe Ile Gly Gly Ser Leu Val Ala Gly Gln Gln				
385	390	395		
ctg aca ggg gga gac ctc atg tcc ttc ctg gtg gcc tcc cag aca gtg				1308
Leu Thr Gly Gly Asp Leu Met Ser Phe Leu Val Ala Ser Gln Thr Val				
400	405	410		
caa agg ctg tgacattcca tgcattggaag gaccatcctt gacaggctgt gtg				1360
Gln Arg Leu				
415				
agctgccctt ccccatgcct gccacttcca gggatgacaa gctgaccctt gtccccacac				1420
acccccacct tatagcttat tgetttagct tgggtccaaaa ccaccgcctc agctgagcct				1480
ctgggatgac cagagctgat caccagacag ctcaaggcgg gcctcccccc tectatctct				1540
ttccaagcta aacacaagca gttctacata aatatgttat ggtaaataat gagatagtaa				1600

139/233

atatgctgta acagatc

1617

<210> 84

<211> 3269

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (260)...(2209)

<400> 84

```

agagtttccg caccggggag ggagatgagg cgggggctca ggctccttgc agttgtaatt      60
tagattcgag aagtggttta tcctttgact ggaaaagaaa agtagctgca gtattccccc      120
agcacttget gagagcatgc cgtatgccag gctgtgaggc tcgagagaca agcagtggaa      180
gagttggggc ctgtttcacc tctggattgt aaatctgagc ctcttctggg cccctggaag      240
gggacagcat cacgatgga atg att cct aac cag cat aat gct gga gcc ggg      292
          Met Ile Pro Asn Gln His Asn Ala Gly Ala Gly
                1             5             10
agc cac caa cct gca gtt ttc aga atg gcc gtg ttg gac act gat ttg      340
Ser His Gln Pro Ala Val Phe Arg Met Ala Val Leu Asp Thr Asp Leu
                15             20             25
gat cac att ctt cca tct tct gtt ctt cct cca ttc tgg gct aag tta      388
Asp His Ile Leu Pro Ser Ser Val Leu Pro Pro Phe Trp Ala Lys Leu
                30             35             40
gta gtg gga tcg gtt gcc att gtg tgt ttt gca cgc agc tat gat gga      436
Val Val Gly Ser Val Ala Ile Val Cys Phe Ala Arg Ser Tyr Asp Gly
                45             50             55
gac ttt gtc ttt gat gac tca gaa gct att gtt aac aat aag gtt gct      484
Asp Phe Val Phe Asp Asp Ser Glu Ala Ile Val Asn Asn Lys Val Ala
                60             65             70             75
ggg gtt gtc ggc cgt gca gac ctc ctg tgt gcc ctg ttc ttc ttg tta      532
Gly Val Val Gly Arg Ala Asp Leu Leu Cys Ala Leu Phe Phe Leu Leu
                80             85             90
tct ttc ctt ggc tac tgt aaa gca ttt aga gaa agt aac aag gag gga      580
Ser Phe Leu Gly Tyr Cys Lys Ala Phe Arg Glu Ser Asn Lys Glu Gly
                95             100             105

```

140/233

gcg cat tct tcc acc ttc tgg gtg ctg ctg agt atc ttt ctg gga gca	628
Ala His Ser Ser Thr Phe Trp Val Leu Leu Ser Ile Phe Leu Gly Ala	
110 115 120	
gtg gcc atg ctg tgc aaa gag caa ggg atc act gtg ctg ggt tta aat	676
Val Ala Met Leu Cys Lys Glu Gln Gly Ile Thr Val Leu Gly Leu Asn	
125 130 135	
gcg gta ttt gac atc ttg gtg ata ggc aaa ttc aat gtt ctg gaa att	724
Ala Val Phe Asp Ile Leu Val Ile Gly Lys Phe Asn Val Leu Glu Ile	
140 145 150 155	
gtc cag aag gta cta cat aag gac aag tca tta gag aat ctc ggc atg	772
Val Gln Lys Val Leu His Lys Asp Lys Ser Leu Glu Asn Leu Gly Met	
160 165 170	
ctc agg aac ggg ggc ctc ctc ttc aga atg acc ctg ctc acc tct gga	820
Leu Arg Asn Gly Gly Leu Leu Phe Arg Met Thr Leu Leu Thr Ser Gly	
175 180 185	
ggg gct ggg atg ctc tac gtg cgc tgg agg atc atg ggc acg ggc ccg	868
Gly Ala Gly Met Leu Tyr Val Arg Trp Arg Ile Met Gly Thr Gly Pro	
190 195 200	
ccg gcc ttc acc gag gtg gac aac ccg gcc tcc ttt gct gac agc atg	916
Pro Ala Phe Thr Glu Val Asp Asn Pro Ala Ser Phe Ala Asp Ser Met	
205 210 215	
ctg gtg agg gcc gta aac tac aat tac tac tat tca ttg aat gcc tgg	964
Leu Val Arg Ala Val Asn Tyr Asn Tyr Tyr Tyr Ser Leu Asn Ala Trp	
220 225 230 235	
ctg ctg ctg tgt ccc tgg tgg ctg tgt ttt gat tgg tca atg ggc tgc	1012
Leu Leu Leu Cys Pro Trp Trp Leu Cys Phe Asp Trp Ser Met Gly Cys	
240 245 250	
atc ccc ctc att aag tcc atc agc gac tgg agg gta att gca ctt gca	1060
Ile Pro Leu Ile Lys Ser Ile Ser Asp Trp Arg Val Ile Ala Leu Ala	
255 260 265	
gca ctc tgg ttc tgc cta att ggc ctg ata tgc caa gcc ctg tgc tct	1108
Ala Leu Trp Phe Cys Leu Ile Gly Leu Ile Cys Gln Ala Leu Cys Ser	
270 275 280	
gaa gac ggc cac aag aga agg atc ctt act ctg ggc ctg gga ttt ctc	1156
Glu Asp Gly His Lys Arg Arg Ile Leu Thr Leu Gly Leu Gly Phe Leu	

141/233

285	290	295	
gtt atc cca ttt ctc ccc gcg agt aac ctg ttc ttc cga gtg ggc ttc			1204
Val Ile Pro Phe Leu Pro Ala Ser Asn Leu Phe Phe Arg Val Gly Phe			
300	305	310	315
gtg gtc gcg gag cgt gtc ctc tac ctc ccc agc att ggg tac tgt gtg			1252
Val Val Ala Glu Arg Val Leu Tyr Leu Pro Ser Ile Gly Tyr Cys Val			
320	325	330	
ctg ctg act ttt gga ttc gga gcc ctg agc aaa cat acc aag aaa aag			1300
Leu Leu Thr Phe Gly Phe Gly Ala Leu Ser Lys His Thr Lys Lys Lys			
335	340	345	
aaa ctc att gcc gct gtc gtg ctg gga atc tta ttc atc aac acg ctg			1348
Lys Leu Ile Ala Ala Val Val Leu Gly Ile Leu Phe Ile Asn Thr Leu			
350	355	360	
aga tgt gtg ctg cgc agc ggc gag tgg cgg agt gag gaa cag ctt ttc			1396
Arg Cys Val Leu Arg Ser Gly Glu Trp Arg Ser Glu Glu Gln Leu Phe			
365	370	375	
aga agt gct ctg tct gtg tgt ccc ctc aat gct aag gtt cac tac aac			1444
Arg Ser Ala Leu Ser Val Cys Pro Leu Asn Ala Lys Val His Tyr Asn			
380	385	390	395
att ggc aaa aac ctg gct gat aaa ggc aac cag aca gct gcc atc aga			1492
Ile Gly Lys Asn Leu Ala Asp Lys Gly Asn Gln Thr Ala Ala Ile Arg			
400	405	410	
tac tac cgg gaa gct gta aga tta aat ccc aag tat gtt cat gcc atg			1540
Tyr Tyr Arg Glu Ala Val Arg Leu Asn Pro Lys Tyr Val His Ala Met			
415	420	425	
aat aat ctt gga aat atc tta aaa gaa agg aat gag cta cag gaa gct			1588
Asn Asn Leu Gly Asn Ile Leu Lys Glu Arg Asn Glu Leu Gln Glu Ala			
430	435	440	
gag gag ctg ctg tct ttg gct gtt caa ata cag cca gac ttt gcc gct			1636
Glu Glu Leu Leu Ser Leu Ala Val Gln Ile Gln Pro Asp Phe Ala Ala			
445	450	455	
gcg tgg atg aat cta ggc ata gtg cag aat agc ctg aaa cgg ttt gaa			1684
Ala Trp Met Asn Leu Gly Ile Val Gln Asn Ser Leu Lys Arg Phe Glu			
460	465	470	475
gca gca gag caa agt tac cgg aca gca att aaa cac aga agg aaa tac			1732

142/233

Ala Ala Glu Gln Ser Tyr Arg Thr Ala Ile Lys His Arg Arg Lys Tyr	
480 485 490	
cca gac tgt tac tac aac ctc ggg cgt ctg tat gca gat ctc aat cgc	1780
Pro Asp Cys Tyr Tyr Asn Leu Gly Arg Leu Tyr Ala Asp Leu Asn Arg	
495 500 505	
cac gtg gat gcc ttg aat gcg tgg aga aat gcc acc gtg ctg aaa cca	1828
His Val Asp Ala Leu Asn Ala Trp Arg Asn Ala Thr Val Leu Lys Pro	
510 515 520	
gag cac agc ctg gcc tgg aac aac atg att ata ctc ctc gac aat aca	1876
Glu His Ser Leu Ala Trp Asn Asn Met Ile Ile Leu Leu Asp Asn Thr	
525 530 535	
ggg aat tta gcc caa gct gaa gca gtt gga aga gag gca ctg gaa tta	1924
Gly Asn Leu Ala Gln Ala Glu Ala Val Gly Arg Glu Ala Leu Glu Leu	
540 545 550 555	
ata cct aat gat cac tct ctc atg ttc tcg ttg gca aac gtg ctg ggg	1972
Ile Pro Asn Asp His Ser Leu Met Phe Ser Leu Ala Asn Val Leu Gly	
560 565 570	
aaa tcc cag aaa tac aag gaa tct gaa gct tta ttc ctc aag gca att	2020
Lys Ser Gln Lys Tyr Lys Glu Ser Glu Ala Leu Phe Leu Lys Ala Ile	
575 580 585	
aaa gca aat cca aat gct gca agt tac cat ggt aat ttg gct gtg ctt	2068
Lys Ala Asn Pro Asn Ala Ala Ser Tyr His Gly Asn Leu Ala Val Leu	
590 595 600	
tat cat cgt tgg gga cat cta gac ttg gcc aag aaa cac tat gaa atc	2116
Tyr His Arg Trp Gly His Leu Asp Leu Ala Lys Lys His Tyr Glu Ile	
605 610 615	
tcc ttg cag ctt gac ccc acg gca tca gga act aag gag aat tac ggt	2164
Ser Leu Gln Leu Asp Pro Thr Ala Ser Gly Thr Lys Glu Asn Tyr Gly	
620 625 630 635	
ctg ctg aga aga aag cta gaa cta atg caa aag aaa gct gtc tgat	2210
Leu Leu Arg Arg Lys Leu Glu Leu Met Gln Lys Lys Ala Val	
640 645	
cctgtttcct tcatgttttg agtttgagtg tgtgtgtgca tgaggcatat cattaatagt	2270
atgtgggttac atttaaccat ttaaaagtct tagacatggtt attttactga tttttttcta	2330
tgaaaacaaa gacatgcaaa aagattatag caccagcaat atactcttga atgcgtgata	2390

143/233

```

tgattttttca ttgaaattgt atttttttcag acaactcaaa tgtaattcta aaattccaaa 2450
aatgtctttt ttaattaaac agaaaaagag aaaaaattat cttgagcaac ttttagtaga 2510
attgagctta catttgggat ctgagccttg tctgttatgg actagcacta ttaaacttca 2570
attatgacca agaaaggata cactggcccc tacaatttgt ataaatattg aacatgtota 2630
tatattagca tttttattta atgacaaagc aaattaagtt tttttatctc ttttttttaa 2690
aacaacatac tgtgaacttt gtaaggaaat atttatttgt atttttatgt tttgaatagg 2750
gcaaataatc gaatgaggaa tggaagtttt aacatagtat atctatatgc ttttccccat 2810
aggaagaaat tgactcttgc agtttttggg tgccttgact tgtgcaattt caatacacag 2870
gagattatgt aatgtaatat ttttcataag cggttactat caattgaaag ttcaagccat 2930
gcttttaggca agagcaggca gctcacatc tttatttttg ttacatccaa ggtgaagagg 2990
gcaacacatc tgtgtaagct gctttttagt gtgtttatct gaaggccgtt ttccattttg 3050
cttaatgtaa ctacagacat tatccagaaa atgcaaaatt ttctatcaaa tggagccaca 3110
ttcgggggaat tctgtgtatt tttagaatt gagttgttcc tgcgtgtttt tatttgatcc 3170
aaacaatgtt ttgttttgtt cttctctgta tgcgtgttgac ctaatgattt atgcaatctc 3230
tgtaatttct tatgcagtaa aattactaca caaactage 3269

```

<210> 85

<211> 458

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (66)...(347)

<400> 85

```

acagttcctc tggacttctc tggaccacag tcctctgcca gacccctgcc agacccagtc 60
ccacc atg atc cat ctg ggt cac atc ctc ttc ctg ctt ttg ctc cca gtg 110
      Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Pro Val
          1             5             10             15
get gca get cag acg act cca gga gag aga tca tca ctc cct gcc ttt 158
Ala Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe
          20             25             30
tac cct ggc act tca ggc tct tgt tcc gga tgt ggg tcc ctc tct ctg 206
Tyr Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu
          35             40             45
ccg ctc ctg gca ggc ctc gtg get get gat gcg gtg gca tct ctg ctc 254

```

144/233

Pro Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Ala Ser Leu Leu
 50 55 60
 atc gtg ggg gcg gtg ttc ctg tgc gca cgc cca cgc cgc agc ccc gcc 302
 Ile Val Gly Ala Val Phe Leu Cys Ala Arg Pro Arg Arg Ser Pro Ala
 65 70 75
 caa gaa gat ggc aaa gtc tac atc aac atg cca ggc agg ggc tgaccc 350
 Gln Glu Asp Gly Lys Val Tyr Ile Asn Met Pro Gly Arg Gly
 80 85 90
 tcctgcagct tggacctttg acttctgacc ctctcaccct ggatggtgtg tgggtggcaca 410
 ggaacccccg ccccaacttt tggattgtaa taaaacaatt gaaacacc 458

<210> 86

<211> 1712

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (180)...(1457)

<400> 86

tcccgtggc tagaagaagt cttcaacttcc caggagagcc aaagcgtgtc tggccctagg 60
 tgggaaaaga actggctgtg acctttgccc tgacctggaa gggcccagcc ttgggctgaa 120
 tggcagcacc cagccccgcc cgtccgggtgc tgaccacact gctggtgget ctcttcggc 179
 atg ggc tcc tgg gct gcg gtc aat ggg atc tgg gtg gag cta cct gtg 227
 Met Gly Ser Trp Ala Ala Val Asn Gly Ile Trp Val Glu Leu Pro Val
 1 5 10 15
 gtg gtc aaa gag ctt cca gag ggt tgg agc ctc ccc tct tac gtc tct 275
 Val Val Lys Glu Leu Pro Glu Gly Trp Ser Leu Pro Ser Tyr Val Ser
 20 25 30
 gtg ctt gtg gct ctg ggg aac ctg ggt ctg ctg gtg gtg acc ctc tgg 323
 Val Leu Val Ala Leu Gly Asn Leu Gly Leu Leu Val Val Thr Leu Trp
 35 40 45
 agg agg ctg gcc cca gga aag gac gag cag gtc ccc atc cgg gtg gtg 371
 Arg Arg Leu Ala Pro Gly Lys Asp Glu Gln Val Pro Ile Arg Val Val
 50 55 60
 cag gtg ctg ggc atg gtg ggc aca gcc ctg ctg gcc tct ctg tgg cac 419

145/233

Gln Val Leu Gly Met Val Gly Thr Ala Leu Leu Ala Ser Leu Trp His
 65 70 75 80
 cat gtg gcc cca gtg gca gga cag ttg cat tct gtg gcc ttc tta gca 467
 His Val Ala Pro Val Ala Gly Gln Leu His Ser Val Ala Phe Leu Ala
 85 90 95
 ctg gcc ttt gtg ctg gca ctg gca tgc tgt gcc tcg aat gtc act ttc 515
 Leu Ala Phe Val Leu Ala Leu Ala Cys Cys Ala Ser Asn Val Thr Phe
 100 105 110
 ctg ccc ttc ttg agc cac ctg cca cct cgc ttc tta cgg tca ttc ttc 563
 Leu Pro Phe Leu Ser His Leu Pro Pro Arg Phe Leu Arg Ser Phe Phe
 115 120 125
 ctg ggt caa ggc ctg agt gcc ctg ctg ccc tgc gtg ctg gcc cta gtg 611
 Leu Gly Gln Gly Leu Ser Ala Leu Leu Pro Cys Val Leu Ala Leu Val
 130 135 140
 cag ggt gtg ggc cgc ctc gag tgc ccg cca gcc ccc atc aac ggc acc 659
 Gln Gly Val Gly Arg Leu Glu Cys Pro Pro Ala Pro Ile Asn Gly Thr
 145 150 155 160
 cct ggc ccc ccg ctc gac ttc ctt gag cgt ttt ccc gcc agc acc ttc 707
 Pro Gly Pro Pro Leu Asp Phe Leu Glu Arg Phe Pro Ala Ser Thr Phe
 165 170 175
 ttc tgg gca ctg act gcc ctt ctg gtc gct tca gct gct gcc ttc cag 755
 Phe Trp Ala Leu Thr Ala Leu Leu Val Ala Ser Ala Ala Ala Phe Gln
 180 185 190
 ggt ctt ctg ctg ctg ttg ccg cca cca cca tct gta ccc aca ggg gag 803
 Gly Leu Leu Leu Leu Leu Pro Pro Pro Pro Ser Val Pro Thr Gly Glu
 195 200 205
 tta gga tca ggc ctc cag gtg gga gcc cca gga gca gag gaa gag gtg 851
 Leu Gly Ser Gly Leu Gln Val Gly Ala Pro Gly Ala Glu Glu Glu Val
 210 215 220
 gaa gag tcc tca cca ctg caa gag cca cca agc cag gca gca ggc acc 899
 Glu Glu Ser Ser Pro Leu Gln Glu Pro Pro Ser Gln Ala Ala Gly Thr
 225 230 235 240
 acc cct ggt cca gac cct aag gcc tat cag ctt cta tca gcc cgc agt 947
 Thr Pro Gly Pro Asp Pro Lys Ala Tyr Gln Leu Leu Ser Ala Arg Ser
 245 250 255

146/233

gcc tgc ctg ctg ggc ctg ttg gcc gcc acc aac gcg ctg acc aat ggc	995
Ala Cys Leu Leu Gly Leu Leu Ala Ala Thr Asn Ala Leu Thr Asn Gly	
260 265 270	
gtg ctg cct gcc gtg cag agc ttt tcc tgc tta ccc tac ggg cgt ctg	1043
Val Leu Pro Ala Val Gln Ser Phe Ser Cys Leu Pro Tyr Gly Arg Leu	
275 280 285	
gcc tac cac ctg gct gtg gtg ctg ggc agt gct gcc aat ccc ctg gcc	1091
Ala Tyr His Leu Ala Val Val Leu Gly Ser Ala Ala Asn Pro Leu Ala	
290 295 300	
tgc ttc ctg gcc atg ggt gtg ctg tgc agg tcc ttg gca ggg ctg ggc	1139
Cys Phe Leu Ala Met Gly Val Leu Cys Arg Ser Leu Ala Gly Leu Gly	
305 310 315 320	
ggc ctc tct ctg ctg ggc gtg ttc tgt ggg ggc tac ctg atg gcg ctg	1187
Gly Leu Ser Leu Leu Gly Val Phe Cys Gly Gly Tyr Leu Met Ala Leu	
325 330 335	
gca gtc ctg agc ccc tgc ccg ccc ctg gtg ggc acc tcg gcg ggg gtg	1235
Ala Val Leu Ser Pro Cys Pro Pro Leu Val Gly Thr Ser Ala Gly Val	
340 345 350	
gtc ctc gtg gtg ctg tcg tgg gtg ctg tgt ctt ggc gtg ttc tcc tac	1283
Val Leu Val Val Leu Ser Trp Val Leu Cys Leu Gly Val Phe Ser Tyr	
355 360 365	
gtg aag gtg gca gcc agc tcc ctg ctg cat ggc ggg ggc cgg ccg gca	1331
Val Lys Val Ala Ala Ser Ser Leu Leu His Gly Gly Gly Arg Pro Ala	
370 375 380	
ttg ctg gca gcc ggc gtg gcc atc cag gtg ggc tct ctg ctc ggc gct	1379
Leu Leu Ala Ala Gly Val Ala Ile Gln Val Gly Ser Leu Leu Gly Ala	
385 390 395 400	
gtt gct atg ttc ccc ccg acc agc atc tat cac gtg ttc cac agc aga	1427
Val Ala Met Phe Pro Pro Thr Ser Ile Tyr His Val Phe His Ser Arg	
405 410 415	
aag gac tgt gca gac ccc tgt gac tcc tgagcctggg caggtgggga ccccg	1480
Lys Asp Cys Ala Asp Pro Cys Asp Ser	
420 425	
toooooaacac ctgtctttcc ctcaatgctg ccaccatgcc tgagtgcctg cagcccagga	1540
ggcccgacaca ccggtacact cgtggacacc tacacactcc ataggagatc ctggettcc	1600

147/233

agggtgggca agggcaagga gcaggcttgg agccagggac cagtgggggc ttaggggtaa 1660
 gcccctgagc ctggggaccta catgtgggtt gcgtaataaa acatttgtat tt 1712

<210> 87

<211> 1055

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (53)...(502)

<400> 87

accgggagggc gcgtggggct tgaggccgag aacggccctt gctgccacca ac atg 55

Met

1

gag act ttg tac cgt gtc ccg ttc tta gtg ctc gaa tgt ccc aac ctg 103

Glu Thr Leu Tyr Arg Val Pro Phe Leu Val Leu Glu Cys Pro Asn Leu

5

10

15

aag ctg aag aag ccg ccc tgg ttg cac atg ccg tcg gcc atg act gtg 151

Lys Leu Lys Lys Pro Pro Trp Leu His Met Pro Ser Ala Met Thr Val

20

25

30

tat gct ctg gtg gtg gtg tct tac ttc ctc atc acc gga gga ata att 199

Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile Ile

35

40

45

tat gat gtt att gtt gaa cct cca agt gtc ggt tct atg act gat gaa 247

Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp Glu

50

55

60

65

cat ggg cat cag agg cca gta gct ttc ttg gcc tac aga gta aat gga 295

His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn Gly

70

75

80

caa tat att atg gaa gga ctt gca tcc agc ttc cta ttt aca atg gga 343

Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met Gly

85

90

95

ggg tta ggt ttc ata atc ctg gac cga tcg aat gca cca aat atc cca 391

Gly Leu Gly Phe Ile Ile Leu Asp Arg Ser Asn Ala Pro Asn Ile Pro

100

105

110

148/233

aaa ctc aat aga ttc ctt ctt ctg ttc att gga ttc gtc tgt gtc cta 439
 Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val Leu
 115 120 125
 ttg agt ttt ttc atg gct aga gta ttc atg aga atg aaa ctg ccg ggc 487
 Leu Ser Phe Phe Met Ala Arg Val Phe Met Arg Met Lys Leu Pro Gly
 130 135 140 145
 tat ctg atg ggt tagagtgcct ttgagaagaa atcagtgat actggatttg c 540
 Tyr Leu Met Gly

tcctgtcaat gaagttttaa aggctgtacc aatcctctaa tatgaaatgt ggaaaagaat 600
 gaagagcagc agtaaaagaa atatctagtg aaaaaacagg aagcgtattg aagcttggac 660
 tagaatttct tcttggtatt aaagagacaa gtttatcaca gaattttttt tcctgctggc 720
 ctattgctat accaatgatg ttgagtggca ttttcttttt agtttttcat taaaatatat 780
 tccatatcta caactataat atcaaataaa gtgattattt tttaacaacc tcttaacatt 840
 ttttggagat gacatttctg attttcagaa attaacataa aatccagaag caagattccg 900
 taagctgaga actctggaca gttgatcagc tttacctatg gtgctttgcc ttttaactaga 960
 gtgtgtgatg gtagattatt tcagatatgt atgtaaaact gtttcctgaa caataagatg 1020
 tatgaacgga gcagaaataa atactttttc taatt 1055

<210> 88

<211> 1616

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (222)...(1412)

<400> 88

gagctctcac ggtttcctct ttctgacaa aaagaatatt aatgaaactt tatcatcttg 60
 gtgagaaaag cattctaata gctttattct gacatacggg ggtatggaga gcttgaagga 120
 gtcagagagg tgcccagcta agacctgaat gccatcaccc tccccagggc tctgcagttt 180
 tctcgtggtg aacccttgat ggatttggtg ttgcttgaga a atg gcg atg atc 233
 Met Ala Met Ile

1

gaa ttg ggg ttt gga aga cag aat ttt cat cca tta aag agg aag agt 281
 Glu Leu Gly Phe Gly Arg Gln Asn Phe His Pro Leu Lys Arg Lys Ser

149/233

5	10	15	20	
tca ttg ctg ttg aaa ctc ata gct gtt gtc ttt gct gtg ctt cta ttt				329
Ser Leu Leu Leu Lys Leu Ile Ala Val Val Phe Ala Val Leu Leu Phe				
25	30	35		
tgt gaa ttt tta atc tat tac tta gcg atc ttt cag tgt aat tgg cct				377
Cys Glu Phe Leu Ile Tyr Tyr Leu Ala Ile Phe Gln Cys Asn Trp Pro				
40	45	50		
gaa gtg aaa acc aca gcc tct gat ggt gaa cag acc aca cgt gag cct				425
Glu Val Lys Thr Thr Ala Ser Asp Gly Glu Gln Thr Thr Arg Glu Pro				
55	60	65		
gtg ctc aaa gcc atg ttt ttg gct gac acc cat ttg ctt ggg gaa ttc				473
Val Leu Lys Ala Met Phe Leu Ala Asp Thr His Leu Leu Gly Glu Phe				
70	75	80		
cta ggc cac tgg ctg gac aaa tta cga agg gaa tgg cag atg gag aga				521
Leu Gly His Trp Leu Asp Lys Leu Arg Arg Glu Trp Gln Met Glu Arg				
85	90	95	100	
gcg ttc cag aca gct ctg tgg ttg ctg cag ccg gaa gtc gtc ttc atc				569
Ala Phe Gln Thr Ala Leu Trp Leu Leu Gln Pro Glu Val Val Phe Ile				
105	110	115		
ctg ggg gat atc ttt gat gaa ggg aag tgg agc acc cct gag gcc tgg				617
Leu Gly Asp Ile Phe Asp Glu Gly Lys Trp Ser Thr Pro Glu Ala Trp				
120	125	130		
gcg gat gat gtg gag cgg ttt cag aaa atg ttc aga cac cca agt cat				665
Ala Asp Asp Val Glu Arg Phe Gln Lys Met Phe Arg His Pro Ser His				
135	140	145		
gta cag ctg aag gta gtt gct gga aac cat gac att ggc ttc cat tat				713
Val Gln Leu Lys Val Val Ala Gly Asn His Asp Ile Gly Phe His Tyr				
150	155	160		
gag atg aac aca tac aaa gta gaa cgc ttt gag aaa gtg ttc agc tct				761
Glu Met Asn Thr Tyr Lys Val Glu Arg Phe Glu Lys Val Phe Ser Ser				
165	170	175	180	
gaa aga ctg ttt tct tgg aaa ggc att aac ttt gtg atg gtc aac agc				809
Glu Arg Leu Phe Ser Trp Lys Gly Ile Asn Phe Val Met Val Asn Ser				
185	190	195		
gtg gcg ctg aac ggg gat ggc tgt ggc atc tgc tct gaa aca gaa gca				857

150/233

Val Ala Leu Asn Gly Asp Gly Cys Gly Ile Cys Ser Glu Thr Glu Ala	
200	205 210
gag ctc att gaa gtt tct cac aga ctg aac tgc tcc cga gag gca cgt	905
Glu Leu Ile Glu Val Ser His Arg Leu Asn Cys Ser Arg Glu Ala Arg	
215	220 225
ggc tcc agc cgg tgt gga cct ggg cct ctg ctg ccc acg tct gcc cct	953
Gly Ser Ser Arg Cys Gly Pro Gly Pro Leu Leu Pro Thr Ser Ala Pro	
230	235 240
gtc ctc ctg cag cat tat cct ctg tat cgg aga agt gat gct aac tgt	1001
Val Leu Leu Gln His Tyr Pro Leu Tyr Arg Arg Ser Asp Ala Asn Cys	
245	250 255 260
tct ggg gaa gac gct gct cct gca gag gaa agg gac atc cca ttt aag	1049
Ser Gly Glu Asp Ala Ala Pro Ala Glu Glu Arg Asp Ile Pro Phe Lys	
265	270 275
gag aac tat gac gtg ctt tca cgg gag gca tca caa aag ctg ctg tgg	1097
Glu Asn Tyr Asp Val Leu Ser Arg Glu Ala Ser Gln Lys Leu Leu Trp	
280	285 290
tgg ctc cag ccg cgc ctg gtt ctc agt ggc cac acg cac agc gcc tgc	1145
Trp Leu Gln Pro Arg Leu Val Leu Ser Gly His Thr His Ser Ala Cys	
295	300 305
gag gtg cac cac ggg ggc cga gtc ccc gag ctc agc gtc cca tct ttc	1193
Glu Val His His Gly Gly Arg Val Pro Glu Leu Ser Val Pro Ser Phe	
310	315 320
agt tgg agg aac aga aac aac ccc agt ttc atc atg ggt agc atc acg	1241
Ser Trp Arg Asn Arg Asn Asn Pro Ser Phe Ile Met Gly Ser Ile Thr	
325	330 335 340
ccc aca gac tac acc ctc tcc aag tgc tac ctc cca cgt gag gat gtg	1289
Pro Thr Asp Tyr Thr Leu Ser Lys Cys Tyr Leu Pro Arg Glu Asp Val	
345	350 355
gtt ttg atc atc tac tgt gga gtg gtg ggc ttc ctt gtg gtc ctc aca	1337
Val Leu Ile Ile Tyr Cys Gly Val Val Gly Phe Leu Val Val Leu Thr	
360	365 370
ctc act cac ttt ggg ctt cta gcc tca cct ttt ctt tct ggt ttg aac	1385
Leu Thr His Phe Gly Leu Leu Ala Ser Pro Phe Leu Ser Gly Leu Asn	
375	380 385

151/233

ttg ctc gga aag cgt aag aca aga tgaagagcag gcgccattat a 1430
 Leu Leu Gly Lys Arg Lys Thr Arg

390

395

aatatcaaag cccaagaaat ggaactttgg gcagagatca tgtagaatc aagtggatga 1490
 tgagaccaat tacaggccgt ctctctgcac agcacagaaa ttctcaatca ctgaaatgag 1550
 taactgcaaa ataaatagtt gattgtactg ttctcatgct ataaaagtgg acagggtactc 1610
 tacaac 1616

<210> 89

<211> 1860

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (69)...(1121)

<400> 89

gagaagtgtc gcgtccgtgc gccgcgggct ggggcgggtct caggtgtgcc gaagctctgg 60
 tcagtgcc atg atc cgg cag gag cgc tcc aca tcc tac cag gag ctg 107

Met Ile Arg Gln Glu Arg Ser Thr Ser Tyr Gln Glu Leu

1

5

10

agt gag gag ttg gtc cag gtg gtt gag aac tca gag ctg gca gac gag 155
 Ser Glu Glu Leu Val Gln Val Val Glu Asn Ser Glu Leu Ala Asp Glu

15

20

25

cag gac aag gag acg gtc aga gtc caa ggt ccg ggt atc tta cca ggc 203
 Gln Asp Lys Glu Thr Val Arg Val Gln Gly Pro Gly Ile Leu Pro Gly

30

35

40

45

ctg gac agc gag tcc gcc tcc agc agc atc cgc ttc agc aag gcc tgc 251
 Leu Asp Ser Glu Ser Ala Ser Ser Ser Ile Arg Phe Ser Lys Ala Cys

50

55

60

ctg aag aac gtc ttc tcg gtc cta ctc atc ttc atc tac ctg ctg ctc 299
 Leu Lys Asn Val Phe Ser Val Leu Leu Ile Phe Ile Tyr Leu Leu Leu

65

70

75

atg gct gtg gcc gtc ttc ctg gtc tac cgg acc atc aca gac ttt cgt 347
 Met Ala Val Ala Val Phe Leu Val Tyr Arg Thr Ile Thr Asp Phe Arg

80

85

90

152/233

gag aaa ctc aag cac cct gtc atg tct gtg tct tac aag gaa gtg gat	395
Glu Lys Leu Lys His Pro Val Met Ser Val Ser Tyr Lys Glu Val Asp	
95 100 105	
cgc tat gat gcc cca ggt att gcc ttg tac ccc ggt cag gcc cag ttg	443
Arg Tyr Asp Ala Pro Gly Ile Ala Leu Tyr Pro Gly Gln Ala Gln Leu	
110 115 120 125	
ctc agc tgt aag cac cat tac gag gtc att cct cct ctg aca agc cct	491
Leu Ser Cys Lys His His Tyr Glu Val Ile Pro Pro Leu Thr Ser Pro	
130 135 140	
ggc cag ccg ggt gac atg aat tgc acc acc cag agg atc aac tac acg	539
Gly Gln Pro Gly Asp Met Asn Cys Thr Thr Gln Arg Ile Asn Tyr Thr	
145 150 155	
gac ccc ttc tcc aat cag act gtg aaa tct gcc ctg att gtc cag ggg	587
Asp Pro Phe Ser Asn Gln Thr Val Lys Ser Ala Leu Ile Val Gln Gly	
160 165 170	
ccc cgg gaa gtg aaa aag cgg gag ctg gtc ttc ctc cag ttc cgc ctg	635
Pro Arg Glu Val Lys Lys Arg Glu Leu Val Phe Leu Gln Phe Arg Leu	
175 180 185	
aac aag agt agt gag gac ttc agc gcc att gat tac ctc ctc ttc tct	683
Asn Lys Ser Ser Glu Asp Phe Ser Ala Ile Asp Tyr Leu Leu Phe Ser	
190 195 200 205	
tct ttc cag gag ttc ctg caa agc cca aac agg gta ggc ttc atg cag	731
Ser Phe Gln Glu Phe Leu Gln Ser Pro Asn Arg Val Gly Phe Met Gln	
210 215 220	
gcc tgt gag agt gcc tat tcc agc tgg aag ttc tct ggg ggc ttc cgc	779
Ala Cys Glu Ser Ala Tyr Ser Ser Trp Lys Phe Ser Gly Gly Phe Arg	
225 230 235	
acc tgg gtc aag atg tca ctg gta aag acc aag gag gag gat ggg cgg	827
Thr Trp Val Lys Met Ser Leu Val Lys Thr Lys Glu Glu Asp Gly Arg	
240 245 250	
gaa gca gtg gag ttc cgg cag gag aca agt gtg gtt aac tac att gac	875
Glu Ala Val Glu Phe Arg Gln Glu Thr Ser Val Val Asn Tyr Ile Asp	
255 260 265	
cag agg cca gct gcc aaa aaa agt gct caa ttg ttt ttt gtg gtc ttt	923
Gln Arg Pro Ala Ala Lys Lys Ser Ala Gln Leu Phe Phe Val Val Phe	

153/233

270	275	280	285	
gaa tgg aaa gat cct ttc atc cag aaa gtc caa gat ata gtc act gcc				971
Glu Trp Lys Asp Pro Phe Ile Gln Lys Val Gln Asp Ile Val Thr Ala				
	290	295	300	
aat cct tgg aac aca att gct ctt ctc tgt ggc gcc ttc ttg gca tta				1019
Asn Pro Trp Asn Thr Ile Ala Leu Leu Cys Gly Ala Phe Leu Ala Leu				
	305	310	315	
ttt aaa gca gca gag ttt gcc aaa ctg agt ata aaa tgg atg atc aaa				1067
Phe Lys Ala Ala Glu Phe Ala Lys Leu Ser Ile Lys Trp Met Ile Lys				
	320	325	330	
att aga aag aga tac ctt aaa aga aga ggt cag gca acg agc cac ata				1115
Ile Arg Lys Arg Tyr Leu Lys Arg Arg Gly Gln Ala Thr Ser His Ile				
	335	340	345	
agc tgaagtcacc tcgcgttggt tagagaactg tccacatcaa tgggagctgt ca				1170
Ser				
350				
tcacttccac tttgtaaagc gagctatcaa caatcctgta ctcaacttgaa gaaatggggc				1230
cttgctggga ggaacagcat gtaaaactgg aacttctaac cccgtcccaa aagaggcggc				1290
gtagagccta atagaagaga ctaatggata aacctacaag ttattttaat atttaaatta				1350
ttaataaact ttttaaagag ctggccaatg acttttgaat agggtttgta gaagatgcct				1410
ttcttcctgt ttggttcatt gtattgtatt aggttaagct ctactagggc aatgaaggct				1470
ctacttttca ctttttaaaa gtggacaaaa gagtgtgatt ttctttttcc aaaaattcct				1530
gagtatcaag acgtgcaggc catgctttgg agcctatgca ctgtacacaa aggcaaaacc				1590
ctatgacttt ggcacatctt gccattgatg tccagcctct gacatgctct ttgatttggt				1650
aaatgttaaa tgagacttta aggctactag aaactagtaa ttaagtttct taatggactg				1710
agtagccacc tacttgccg gctagaatgt ttgttgatgt atgagtttag attaacactc				1770
aaaagcacta ggacagatgt acatagaagg tgcctactca ttgtattttg atgatttcat				1830
taacaggtaa ataaaagta atacaaaagg				1860

<210> 90

<211> 783

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

154/233

<222> (245)...(706)

<400> 90

acacacccag tgaggtctct ggagccgcgg tgcgggaagc ggggacccgg gtttgaatcc	60
tgccctctctg gtgtggtgcg gcctcttccc acagactttt ggctcagtg ttccccgcct	120
gggaagtggg gactggccct ggtacctggc tccagagctg caccagagg cgatcagccc	180
ggtgcgggaa cggggcgggg tggccgcaac tacgggccac ggatcctgac ccgccctgcc	240
cacg atg act atc cac atc ctc atc ctg ctg ttg ctc ctc gcc ttc	286
Met Thr Ile His Ile Leu Ile Leu Leu Leu Leu Ala Phe	
1 5 10	
tcc gcc caa ggg gac ctg gac act gca gcc agg cga ggc cag cac cag	334
Ser Ala Gln Gly Asp Leu Asp Thr Ala Ala Arg Arg Gly Gln His Gln	
15 20 25 30	
gtc ccc cag cac cgc ggg cac gtc tgc tac ctg ggc gta tgc cgg acc	382
Val Pro Gln His Arg Gly His Val Cys Tyr Leu Gly Val Cys Arg Thr	
35 40 45	
cac cgc ctg gcg gag atc ata tac tgg att cgc tgt ctc cac caa gga	430
His Arg Leu Ala Glu Ile Ile Tyr Trp Ile Arg Cys Leu His Gln Gly	
50 55 60	
gcc ctc ggg gaa ggc cag cca cga gcc cca gga ccc cta cag cta tgg	478
Ala Leu Gly Glu Gly Gln Pro Arg Ala Pro Gly Pro Leu Gln Leu Trp	
65 70 75	
gcg ccg ccg gtg gcg cga ggc gga agc ccg gct cgg ttc cca gga ttc	526
Ala Pro Pro Val Ala Arg Gly Gly Ser Pro Ala Arg Phe Pro Gly Phe	
80 85 90	
cgg cct gca gcg agg ggg cta gcg cag tgc cca gct cgc tgg gtg acc	574
Arg Pro Ala Ala Arg Gly Leu Ala Gln Cys Pro Ala Arg Trp Val Thr	
95 100 105 110	
tcg ggc acg gct cgt ccc ctc ctc ggc ttc agt ttg cct atc tgt atg	622
Ser Gly Thr Ala Arg Pro Leu Leu Gly Phe Ser Leu Pro Ile Cys Met	
115 120 125	
ttg gag ctt cta ctc cac att tct tct ccc cta act cca gcc cct gaa	670
Leu Glu Leu Leu Leu His Ile Ser Ser Pro Leu Thr Pro Ala Pro Glu	
130 135 140	
acc gtc ttc ccc agt ccc tcc ccg ggc tgc gac taggttggaag ctagaag	720
Thr Val Phe Pro Ser Pro Ser Pro Gly Cys Asp	

155/233

145

150

cacacgggac caggetgggc gaagaacact gacgccccaga gccgaataaa caagagttcc 780
gtg 783

<210> 91

<211> 303

<212> PRT

<213> Homo sapiens

<400> 91

Met Glu Ala Glu Gln Arg Pro Ala Ala Gly Ala Ser Glu Gly Ala Thr
1 5 10 15
Pro Gly Leu Glu Ala Val Pro Pro Val Ala Pro Pro Pro Ala Thr Ala
20 25 30
Ala Ser Gly Pro Ile Pro Lys Ser Gly Pro Glu Pro Lys Arg Arg His
35 40 45
Leu Gly Thr Leu Leu Gln Pro Thr Val Asn Lys Phe Ser Leu Arg Val
50 55 60
Phe Gly Ser His Lys Ala Val Glu Ile Glu Gln Glu Arg Val Lys Ser
65 70 75 80
Ala Gly Ala Trp Ile Ile His Pro Tyr Ser Asp Phe Arg Phe Tyr Trp
85 90 95
Asp Leu Ile Met Leu Leu Leu Met Val Gly Asn Leu Ile Val Leu Pro
100 105 110
Val Gly Ile Thr Phe Phe Lys Glu Glu Asn Ser Pro Pro Trp Ile Val
115 120 125
Phe Asn Val Leu Ser Asp Thr Phe Phe Leu Leu Asp Leu Val Leu Asn
130 135 140
Phe Arg Thr Gly Ile Val Val Glu Glu Gly Ala Glu Ile Leu Leu Ala
145 150 155 160
Pro Arg Ala Ile Arg Thr Arg Tyr Leu Arg Thr Trp Phe Leu Val Asp
165 170 175
Leu Ile Ser Ser Ile Pro Val Asp Tyr Ile Phe Leu Val Val Glu Leu
180 185 190
Glu Pro Arg Leu Asp Ala Glu Val Tyr Lys Thr Ala Arg Ala Leu Arg
195 200 205

156/233

Ile Val Arg Phe Thr Lys Ile Leu Ser Leu Leu Arg Leu Leu Arg Leu
 210 215 220
 Ser Arg Leu Ile Arg Tyr Ile His Gln Trp Glu Glu Ile Phe His Met
 225 230 235 240
 Thr Tyr Asp Leu Ala Ser Ala Val Val Arg Ile Phe Asn Leu Ile Gly
 245 250 255
 Met Met Leu Leu Leu Cys His Trp Asp Gly Cys Leu Gln Phe Leu Val
 260 265 270
 Pro Met Leu Gln Asp Phe Pro Pro Asp Cys Trp Val Ser Ile Asn His
 275 280 285
 Met Val Val Arg Ser Pro His Ser Ser Ala Phe Pro Gly Pro Ser
 290 295 300

<210> 92

<211> 283

<212> PRT

<213> Homo sapiens

<400> 92

Met Ala Asp Pro His Gln Leu Phe Asp Asp Thr Ser Ser Ala Gln Ser
 1 5 10 15
 Arg Gly Tyr Gly Ala Gln Arg Ala Pro Gly Gly Leu Ser Tyr Pro Ala
 20 25 30
 Ala Ser Pro Thr Pro His Ala Ala Phe Leu Ala Asp Pro Val Ser Asn
 35 40 45
 Met Ala Met Ala Tyr Gly Ser Ser Leu Ala Ala Gln Gly Lys Glu Leu
 50 55 60
 Val Asp Lys Asn Ile Asp Arg Phe Ile Pro Ile Thr Lys Leu Lys Tyr
 65 70 75 80
 Tyr Phe Ala Val Asp Thr Met Tyr Val Gly Arg Lys Leu Gly Leu Leu
 85 90 95
 Phe Phe Pro Tyr Leu His Gln Asp Trp Glu Val Gln Tyr Gln Gln Asp
 100 105 110
 Thr Pro Val Ala Pro Arg Phe Asp Val Asn Ala Pro Asp Leu Tyr Ile
 115 120 125
 Pro Ala Met Ala Phe Ile Thr Tyr Val Leu Val Ala Gly Leu Ala Leu

130					135					140					
Gly	Thr	Gln	Asp	Arg	Phe	Ser	Pro	Asp	Leu	Leu	Gly	Leu	Gln	Ala	Ser
145					150					155					160
Ser	Ala	Leu	Ala	Trp	Leu	Thr	Leu	Glu	Val	Leu	Ala	Ile	Leu	Leu	Ser
165					170					175					
Leu	Tyr	Leu	Val	Thr	Val	Asn	Thr	Asp	Leu	Thr	Thr	Ile	Asp	Leu	Val
180					185					190					
Ala	Phe	Leu	Gly	Tyr	Lys	Tyr	Val	Gly	Met	Ile	Gly	Gly	Val	Leu	Met
195					200					205					
Gly	Leu	Leu	Phe	Gly	Lys	Ile	Gly	Tyr	Tyr	Leu	Val	Leu	Gly	Trp	Cys
210					215					220					
Cys	Val	Ala	Ile	Phe	Val	Phe	Met	Ile	Arg	Thr	Leu	Arg	Leu	Lys	Ile
225					230					235					240
Leu	Ala	Asp	Ala	Ala	Ala	Glu	Gly	Val	Pro	Val	Arg	Gly	Ala	Arg	Asn
245					250					255					
Gln	Leu	Arg	Met	Tyr	Leu	Thr	Met	Ala	Val	Ala	Ala	Ala	Gln	Pro	Met
260					265					270					
Leu	Met	Tyr	Trp	Leu	Thr	Phe	His	Leu	Val	Arg					
275					280										

Met	Ala	Gly	Lys	Gly	Ser	Ser	Gly	Arg	Arg	Pro	Leu	Leu	Leu	Gly	Leu
1				5					10					15	
Leu	Val	Ala	Val	Ala	Thr	Val	His	Leu	Val	Ile	Cys	Pro	Tyr	Thr	Lys
			20					25					30		
Val	Glu	Glu	Ser	Phe	Asn	Leu	Gln	Ala	Thr	His	Asp	Leu	Leu	Tyr	His
		35					40					45			
Trp	Gln	Asp	Leu	Glu	Gln	Tyr	Asp	His	Leu	Glu	Phe	Pro	Gly	Val	Val
50						55					60				
Pro	Arg	Thr	Phe	Leu	Gly	Pro	Val	Val	Ile	Ala	Val	Phe	Ser	Ser	Pro
65				70						75				80	

158/233

Ala Val Tyr Val Leu Ser Leu Leu Glu Met Ser Lys Phe Tyr Ser Gln
 85 90 95
 Leu Ile Val Arg Gly Val Leu Gly Leu Gly Val Ile Phe Gly Leu Trp
 100 105 110
 Thr Leu Gln Lys Glu Val Arg Arg His Phe Gly Ala Met Val Ala Thr
 115 120 125
 Met Phe Cys Trp Val Thr Ala Met Gln Phe His Leu Met Phe Tyr Cys
 130 135 140
 Thr Arg Thr Leu Pro Asn Val Leu Ala Leu Pro Val Val Leu Leu Ala
 145 150 155 160
 Leu Ala Ala Trp Leu Arg His Glu Trp Ala Arg Phe Ile Trp Leu Ser
 165 170 175
 Ala Phe Ala Ile Ile Val Phe Arg Val Glu Leu Cys Leu Phe Leu Gly
 180 185 190
 Leu Leu Leu Leu Leu Ala Leu Gly Asn Arg Lys Val Ser Val Val Arg
 195 200 205
 Ala Leu Arg His Ala Val Pro Ala Gly Ile Leu Cys Leu Gly Leu Thr
 210 215 220
 Val Ala Val Asp Ser Tyr Phe Trp Arg Gln Leu Thr Trp Pro Glu Gly
 225 230 235 240
 Lys Val Leu Trp Tyr Asn Thr Val Leu Asn Lys Ser Ser Asn Trp Gly
 245 250 255
 Thr Ser Pro Leu Leu Trp Tyr Phe Tyr Ser Ala Leu Pro Arg Gly Leu
 260 265 270
 Gly Cys Ser Leu Leu Phe Ile Pro Leu Gly Leu Val Asp Arg Arg Thr
 275 280 285
 His Ala Pro Thr Val Leu Ala Leu Gly Phe Met Ala Leu Tyr Ser Leu
 290 295 300
 Leu Pro His Lys Glu Leu Arg Phe Ile Ile Tyr Ala Phe Pro Met Leu
 305 310 315 320
 Asn Ile Thr Ala Ala Arg Gly Cys Ser Tyr Leu Leu Asn Asn Tyr Lys
 325 330 335
 Lys Ser Trp Leu Tyr Lys Ala Gly Ser Leu Leu Val Ile Gly His Leu
 340 345 350
 Val Val Asn Ala Ala Tyr Ser Ala Thr Ala Leu Tyr Val Ser His Phe

159/233

355 360 365
 Asn Tyr Pro Gly Gly Val Ala Met Gln Arg Leu His Gln Leu Val Pro
 370 375 380
 Pro Gln Thr Asp Val Leu Leu His Ile Asp Val Ala Ala Ala Gln Thr
 385 390 395 400
 Gly Val Ser Arg Phe Leu Gln Val Asn Ser Ala Trp Arg Tyr Asp Lys
 405 410 415
 Arg Glu Asp Val Gln Pro Gly Thr Gly Met Leu Ala Tyr Thr His Ile
 420 425 430
 Leu Met Glu Ala Ala Pro Gly Leu Leu Ala Leu Tyr Arg Asp Thr His
 435 440 445
 Arg Val Leu Ala Ser Val Val Gly Thr Thr Gly Val Ser Leu Asn Leu
 450 455 460
 Thr Gln Leu Pro Pro Phe Asn Val His Leu Gln Thr Lys Leu Val Leu
 465 470 475 480
 Leu Glu Arg Leu Pro Arg Pro Ser
 485

<210> 94

<211> 182

<212> PRT

<213> Homo sapiens

<400> 94

Met Trp Pro Pro Asp Pro Asp Pro Asp Pro Glu Pro Ala Gly
 1 5 10 15
 Gly Ser Arg Pro Gly Pro Ala Val Pro Gly Leu Arg Ala Leu Leu Pro
 20 25 30
 Ala Arg Ala Phe Leu Cys Ser Leu Lys Gly Arg Leu Leu Leu Ala Glu
 35 40 45
 Ser Gly Leu Ser Phe Ile Thr Phe Ile Cys Tyr Val Ala Ser Ser Ala
 50 55 60
 Ser Ala Phe Leu Thr Ala Pro Leu Leu Glu Phe Leu Leu Ala Leu Tyr
 65 70 75 80
 Phe Leu Phe Ala Asp Ala Met Gln Leu Asn Asp Lys Trp Gln Gly Leu
 85 90 95

160/233

Cys Trp Pro Met Met Asp Phe Leu Arg Cys Val Thr Ala Ala Leu Ile
 100 105 110
 Tyr Phe Ala Ile Ser Ile Thr Ala Ile Ala Lys Tyr Ser Asp Gly Ala
 115 120 125
 Ser Lys Ala Ala Gly Val Phe Gly Phe Phe Ala Thr Ile Val Phe Ala
 130 135 140
 Thr Asp Phe Tyr Leu Ile Phe Asn Asp Val Ala Lys Phe Leu Lys Gln
 145 150 155 160
 Gly Asp Ser Ala Asp Glu Thr Thr Ala His Lys Thr Glu Glu Glu Asn
 165 170 175
 Ser Asp Ser Asp Ser Asp
 180

<210> 95

<211> 184

<212> PRT

<213> Homo sapiens

<400> 95

Met Asp Gly Leu Arg Gln Arg Val Glu His Phe Leu Glu Gln Arg Asn
 1 5 10 15
 Leu Val Thr Glu Val Leu Gly Ala Leu Glu Ala Lys Thr Gly Val Glu
 20 25 30
 Lys Arg Tyr Leu Ala Ala Gly Ala Val Thr Leu Leu Ser Leu Tyr Leu
 35 40 45
 Leu Phe Gly Tyr Gly Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe Val
 50 55 60
 Tyr Pro Ala Tyr Ala Ser Ile Lys Ala Ile Glu Ser Pro Ser Lys Asp
 65 70 75 80
 Asp Asp Thr Val Trp Leu Thr Tyr Trp Val Val Tyr Ala Leu Phe Gly
 85 90 95
 Leu Ala Glu Phe Phe Ser Asp Leu Leu Leu Ser Trp Phe Pro Phe Tyr
 100 105 110
 Tyr Val Gly Lys Cys Ala Phe Leu Leu Phe Cys Met Ala Pro Arg Pro
 115 120 125
 Trp Asn Gly Ala Leu Met Leu Tyr Gln Arg Val Val Arg Pro Leu Phe

161/233

130 135 140
 Leu Arg His His Gly Ala Val Asp Arg Ile Met Asn Asp Leu Ser Gly
 145 150 155 160
 Arg Ala Leu Asp Ala Ala Ala Gly Ile Thr Arg Asn Val Lys Pro Ser
 165 170 175
 Gln Thr Pro Gln Pro Lys Asp Lys
 180

<210> 96

<211> 140

<212> PRT

<213> Homo sapiens

<400> 96

Met Ser Arg Phe Leu Asn Val Leu Arg Ser Trp Leu Val Met Val Ser
 1 5 10 15
 Ile Ile Ala Met Gly Asn Thr Leu Gln Ser Phe Arg Asp His Thr Phe
 20 25 30
 Leu Tyr Glu Lys Leu Tyr Thr Gly Lys Pro Asn Leu Val Asn Gly Leu
 35 40 45
 Gln Ala Arg Thr Phe Gly Ile Trp Thr Leu Leu Ser Ser Val Ile Arg
 50 55 60
 Cys Leu Cys Ala Ile Asp Ile His Asn Lys Thr Leu Tyr His Ile Thr
 65 70 75 80
 Leu Trp Thr Phe Leu Leu Ala Leu Gly His Phe Leu Ser Glu Leu Phe
 85 90 95
 Val Tyr Gly Thr Ala Ala Pro Thr Ile Gly Val Leu Ala Pro Leu Met
 100 105 110
 Val Ala Ser Phe Ser Ile Leu Gly Met Leu Val Gly Leu Arg Tyr Leu
 115 120 125
 Glu Val Glu Pro Val Ser Arg Gln Lys Lys Arg Asn
 130 135 140

<210> 97

<211> 153

<212> PRT

162/233

<213> Homo sapiens

<400> 97

Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg Val
 1 5 10 15
 Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly Leu
 20 25 30
 Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val Ala
 35 40 45
 Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe Leu
 50 55 60
 His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys Ala
 65 70 75 80
 Arg Leu Leu Thr His Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe Thr
 85 90 95
 Ser Ser Arg Lys Phe Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe Leu
 100 105 110
 Ala Ser Phe Tyr Thr Lys Tyr Asp Pro Thr His Phe Ile Leu Asn Thr
 115 120 125
 Ala Ser Leu Leu Ser Val Leu Ile Pro Lys Met Pro Gln Leu His Gly
 130 135 140
 Val Arg Ile Phe Gly Ile Asn Lys Tyr
 145 150

<210> 98

<211> 173

<212> PRT

<213> Homo sapiens

<400> 98

Met Ala Ala Phe Leu Ile Gln Thr Lys Asp Asn Pro Met Lys Ala Val
 1 5 10 15
 Gly Val Leu Ala Gly Thr Met Ala Thr Val Val Ala Ile Thr Val Leu
 20 25 30
 Ile Ser Thr Ala Thr Phe Trp Arg Asn Lys Lys Ser Asn Lys Val Leu
 35 40 45
 Pro Met Arg Arg Val Leu Arg Lys Arg Pro Ser Pro Ala Pro Arg Thr

163/233

50 55 60
 Ile Arg Ile Glu Trp Leu Lys Ser Lys Ser Thr Lys Ala Ala Thr Lys
 65 70 75 80
 Phe Met Leu Lys Glu Lys Pro Pro Asn Glu Asn Cys Asn Asn Asn Ser
 85 90 95
 Pro Glu Ser Ser Leu Leu Pro Arg Ala Pro Ala Leu Pro Pro Pro Pro
 100 105 110
 Ser Val Ala Pro Ser Thr Gly Ala Ala Gln Trp Thr Val Pro Thr Val
 115 120 125
 Ser Gly Ser Leu Thr Pro Gln Pro Thr Gln Pro Pro Pro Lys Pro Lys
 130 135 140
 Thr Met Gly Ser Pro Val Gln Ser Thr Leu Ile Ser Glu Leu Lys Gln
 145 150 155 160
 Lys Phe Glu Lys Lys Ser Val His Asn Lys Ala Tyr Phe
 165 170

<210> 99

<211> 75

<212> PRT

<213> Homo sapiens

<400> 99

Met Ile Gly Asp Ile Leu Leu Phe Gly Thr Leu Leu Met Asn Ala Gly
 1 5 10 15
 Ala Val Leu Asn Phe Lys Leu Lys Lys Lys Asp Thr Gln Gly Phe Gly
 20 25 30
 Glu Glu Ser Arg Glu Pro Ser Thr Gly Asp Asn Ile Arg Glu Phe Leu
 35 40 45
 Leu Ser Leu Arg Tyr Phe Arg Ile Phe Ile Ala Leu Trp Asn Ile Phe
 50 55 60
 Met Met Phe Cys Met Ile Val Leu Phe Gly Ser
 65 70 75

<210> 100

<211> 159

<212> PRT

164/233

<213> Homo sapiens

<400> 100

Met Glu Leu Pro Ala Val Asn Leu Lys Val Ile Leu Leu Gly His Trp
 1 5 10 15
 Leu Leu Thr Thr Trp Gly Cys Ile Val Phe Ser Gly Ser Tyr Ala Trp
 20 25 30
 Ala Asn Phe Thr Ile Leu Ala Leu Gly Val Trp Ala Val Ala Gln Arg
 35 40 45
 Asp Ser Ile Asp Ala Ile Ser Met Phe Leu Gly Gly Leu Leu Ala Thr
 50 55 60
 Ile Phe Leu Asp Ile Val His Ile Ser Ile Phe Tyr Pro Arg Val Ser
 65 70 75 80
 Leu Thr Asp Thr Gly Arg Phe Gly Val Gly Met Ala Ile Leu Ser Leu
 85 90 95
 Leu Leu Lys Pro Leu Ser Cys Cys Phe Val Tyr His Met Tyr Arg Glu
 100 105 110
 Arg Gly Gly Glu Leu Leu Val His Thr Gly Phe Leu Gly Ser Ser Gln
 115 120 125
 Asp Arg Ser Ala Tyr Gln Thr Ile Asp Ser Ala Glu Ala Pro Ala Asp
 130 135 140
 Pro Phe Ala Val Pro Glu Gly Arg Ser Gln Asp Ala Arg Gly Tyr
 145 150 155

<210> 101

<211> 909

<212> DNA

<213> Homo sapiens

<400> 101

atggaggcag agcagcggcc ggcgggcggg gccagcgaag gggcgacccc tggactggag 60
 gcgggtgcctc ccgttgctcc ccgcctgag accgcggcct caggtccgat ccccaaactc 120
 gggcctgagc ctaagaggag gcaccttggg acgctgctcc agcctacggt caacaagttc 180
 tcccttcggg tgttcggcag ccacaaagca gtggaaatcg agcaggagcg ggtgaagtca 240
 gcgggggcct ggatcatcca cccctacagc gaacttcgggt tttactggga cctgatcatg 300
 ctgctgctga tggtagggaa cctcatcgtc ctgcctgtgg gcacacctt cttcaaggag 360
 gagaactccc cgccttggat cgtcttcaac gtattgtctg atactttctt cctactggat 420

165/233

ctggtgctca acttccgaac gggcatcgtg gtggaggagg gtgctgagat cctgctggca	480
ccgcggggcca tccgcacgcg ctacctgogc acctggttcc tggttgacct catctcttct	540
atccctgtgg attacatctt cctagtgggtg gagctggagc cacggttggga cgtgagggtc	600
tacaaaaacgg caccggccct acgcacgtt cgcttcacca agatcctaag cctgctgagg	660
ctgctccgcc tctcccgct catccgtac atacaccagt gggaggagat ctttcacatg	720
acctatgacc tggccagtgc tgtggttcgc atcttcaacc tcattgggat gatgctgctg	780
ctatgtcaact gggatggctg tctgcagttc ctggtgcca tgetgcagga ctccctccc	840
gaetgctggg tctccatcaa ccacatggtg gtgagaagtc cccacagctc tgcctttcct	900
gggccttct	909

<210> 102

<211> 849

<212> DNA

<213> Homo sapiens

<400> 102

atggccgacc cccaccagct ttctgatgac acaagttcag cccagagccg gggctatggg	60
gcccagcggg cactggtgg cctgagttat cctgcagcct ctcccacgcc ccatgcagcc	120
ttcttggtg acccgggtgc caacatggcc atggcctatg ggagcagcct ggccgcgcag	180
ggcaaggagc tgggtgataa gaacatcgac cgcttcaccc ccatcaccaa gctcaagtat	240
tactttgctg tggacaccat gtatgtgggc agaaagctgg gcctgctgtt ctccccctac	300
ctacaccagg actgggaagt gcagtaccaa caggacaccc cgggtggccc cgcctttgac	360
gtcaatgccc cggaccteta cattccagca atggctttca tcacctacgt tttggtggct	420
ggtcttgccg tggggaccca ggataggttc tcccagacc tcctggggct gcaagcgagc	480
tcagccctgg cctggctgac cctggagggtg ctggccatcc tgetcagcct ctatctggtc	540
actgtcaaca ccgacctcac caccatcgac ctggtggcct tcttgggcta caaatatgtc	600
gggatgattg gcggggctct catgggcctg ctcttcggga agattggcta ctacctggtg	660
ctgggctggt gctgcgtagc catctttgtg ttcatgatcc ggacgctgcg gctgaagatc	720
ttggcagacg cagcagctga gggggctccc gtgcgtgggg ccgggaacca gctgcgcagt	780
tacctgacca tggcgggtggc ggccggcgag cctatgetca tgtactggtc cacttccac	840
ctggtgcgg	849

<210> 103

<211> 1464

<212> DNA

<213> Homo sapiens

166/233

<400> 103

atggctggaa aggggtcacc aggcaggcgg cccctgctgc tggggctgct ggtggcggta	60
gccactgtcc acctggatcat ctgtccctac accaaagtgg aggagagctt caacctgcag	120
gccacacatg acctgctcta ccaactggcaa gacctggagc agtacgacca tcttgagttc	180
cccggagtcg tccccaggac gttcctcggg ccagtgggtga tcgcagtgtt ctccagcccc	240
gcggtttacg tgctttcgtt gttagaaatg tccaagtttt actctcagct aatagttaga	300
ggagtgtctg gactcggcgt gattttttgga ctctggacgt tacaaaagga agtgagacgg	360
cacttcgggg ccattggtggc caccatgttc tgctgggtga cggccatgca gttccacctg	420
atgttctact gcacgcggac actgcccaat gtgctggccc tgctgtagt cctgctggcc	480
ctcgcggcct ggtgcgggca cgagtgggccc cgcttcctct ggtgtcagc ctccgccatc	540
atcgtgttca ggggtggagct gtgcctgttc ctgggcctcc tgctgctgct ggccttgggc	600
aaccgaaagg tttctgtagt cagagccctt cgccacgcgg tcccggcagg gatcctctgt	660
ttaggaactga cgggtgtgtt ggactcttat ttttggcggc agctcaactt gcgggaagga	720
aaggtgcttt ggtacaacac tgtcctgaac aaaagctcca actgggggac ctccccgctg	780
ctgtgttact tctactcagc cctgccccgc ggcttgggct gcagcctgct ctccatcccc	840
ctgggcttgg tagacagaag gacgcacgcg ccgacgggtg tggcactggg ctccatggca	900
ctctactccc tctgccaca caaggagcta cgcttcacca totatgcctt ccccatgctc	960
aacatcacgg ctgccagagg ctgctcctac ctgctgaata actataaaaa gtcttggctg	1020
tacaaagcag ggtctctgct tgtgatcgga caccctgtgg tgaatgccgc ctactcagcc	1080
acggccctgt atgtgtccca tttcaactac ccagggtggc tcgcaatgca gaggtgcac	1140
cagctggtgc cccccagac agacgtcctt ctgcacattg acgtggcagc cggccagaca	1200
ggtgtgtctc ggtttctcca agtcaacagc gcctggagggt acgacaagag ggaggatgtg	1260
cagccgggga caggcatgct ggcatacaca cacatcctca tggaggcggc ccctgggctc	1320
ctggccctct acagggacac acaccgggtc ctggccagcg tcgtggggac cacagggtgtg	1380
agtctgaacc tgacccaact gcccccttc aacgtccacc tgcagacaaa gctgggtgctt	1440
ctggagaggg tccccggcc gtcc	1464

<210> 104

<211> 546

<212> DNA

<213> Homo sapiens

<400> 104

atgtggcccc cagacccccga ccccgaccgg gaccccgagc ctgccggcgg ctcccgctcc	60
ggcccccgcg tccccgggtt ccgcgcctct ctgcggcgcc gggctttcct ctgctctctc	120
aaaggccgcc tctgctggc cgagtccggg ctctcattca tcaacttttat ctgctatgtg	180

167/233

gcgtcctcag catctgcctt cctcacagcg cctctgctgg agttcctgct ggccttgtae 240
 ttctcttttg ctgatgccat gcagctgaat gacaagtggc agggcttggt ctggcccatg 300
 atggacttcc tgcgctgtgt caccgcggcc ctcatctact ttgtatctc catcacggcc 360
 atcgccaagt actcggtatg ggcttccaaa gccgctgggg tgtttggctt ctttgtatcc 420
 atcgtgtttg caactgattt ctacctgate tttaacgacg tggccaaatt cctcaaacaa 480
 ggggactctg cagatgagac cacagcccac aagacagaag aagagaattc cgactcggac 540
 tctgac 546

<210> 105

<211> 552

<212> DNA

<213> Homo sapiens

<400> 105

atggacggcc tgaggcagcg cgtggagcac ttctggagc aaaggaacct ggtaaccgaa 60
 gtgctggggg cgtgaggagc caagaccggg gtggagaagc ggtatctggc tgcaggagcc 120
 gtoactctgc taagcctgta tctgctgttc ggctacggag cgtctctgct gtgcaatctc 180
 atcggatttg tgtaccccgcc atatgcctca atcaaagcta tcgagagccc aagcaaggac 240
 gacgacactg tgtggctcacc ctactgggtg gtgtacgccc tgtttgggct ggccgagttc 300
 ttacgcgac tactcctgtc ctgggttccct ttctactacg tgggcaagtg cgccttctctg 360
 ttgtttctgca tggctcccag gccctggaac ggggctctca tgcgttatca gcgcgtcgtg 420
 cgtccgctgt tcctaaggca ccacggggcc gtagacagaa tcatgaacga cctcagcggg 480
 cgagccctgg acgcggcgcc cggaataacc aggaacgtca agccaagcca gaccccgag 540
 ccgaaggaca ag 552

<210> 106

<211> 420

<212> DNA

<213> Homo sapiens

<400> 106

atgagccgtt tcctgaatgt gttaagaagt tggctgggta tgggtgtccat catagccatg 60
 gggaaacacgc tgcagagctt ccgagaccac acttttctct atgaaaagct ctacactggc 120
 aagccaaacc ttgtgaatgg cctccaagct cggacctttg ggatctggac gctgctctca 180
 tcagtgatcc gctgcctctg tgccattgac attcacaaca agacgctcta tcacatcaca 240
 ctctggacct tcctccttgc cctggggcat ttctctctg agttgtttgt ctatggaact 300
 gcagctccca cgattggcgt cctggcacc ctagtggtgg caagtctctc catcctgggt 360

168/233

atgctggtcg ggtccggtat tctagaagta gaaccagtat ccagacagaa gaagagaaac 420

<210> 107

<211> 459

<212> DNA

<213> Homo sapiens

<400> 107

atgaacgttg gagttgcca cagtgaagtg aatccaaata cccgtgtcat gaacagccgg 60
ggtatgtggc tgacatatgc attgggagtt ggttgettc atattgtctt actcagcatt 120
cccttcttca gtgttcctgt tgettggact ttaacaaata ttatacataa tctggggatg 180
tacgtatttt tgcattgcagt gaaaggaaca ccttcgaaa ctctgacca gggtaaagca 240
aggtctctaa ctcatggga acaactggac tatggagtac agtttacatc ttcacggaag 300
tttttcacaa tttctccaat aattctatat tttctggcaa gtttctatac gaagtatgat 360
ccaactcact tcctctaaa cacagcttct ctctgagtg tactaattcc caaaatgcca 420
caactacatg gtgttcggat ctttggaatt aataagtat 459

<210> 108

<211> 519

<212> DNA

<213> Homo sapiens

<400> 108

atggctgctt tcctgataca gaccaaggac aaccccatga aggcctggg tgtgctggcc 60
ggcaccatgg ccacgtcgt ggcatcact gtctcatct ccaccgccac cttctggcgc 120
aacaagaagt ctaacaaggc cctgccaatg cggcgggtgc tccgcaagcg gccagccct 180
gcgccccgca ccattcccat tgagtggctc aagtccaaga gcaccaaagc cgtaccaag 240
ttcatgctca aagagaaacc tcccaatgag aactgtaaca acaacagccc agaaagctct 300
ctgtcccgga gagctccggc tctccctcca ccaccagcg tggcgcccag cactggcgca 360
gccagtgga cgtgcctac tgtctctggc tctctcactc cgcagccgac ccaacccccg 420
ccaaaaccca aaactatggg aagccccgtc cagtcaactc tgatctctga gctcaagcaa 480
aagtttgaga agaagagtgt gcacaacaag gcttacttc 519

<210> 109

<211> 225

<212> DNA

<213> Homo sapiens

169/233

<400> 109

atgatcggag acatcctgct gtccgggacg ttgctgatga atgccggggc ggtgctgaac 60
 ttttaagctga aaaagaagga cacgcagggc tttggggagg agtccagga gccagcaca 120
 ggtgacaaca tccgggaatt cttgctgagc ctcagatact ttcgaatctt catcgccctg 180
 tggaacatct tcatgatgtt ctgcattgatt gtgctgttcg gctct 225

<210> 110

<211> 477

<212> DNA

<213> Homo sapiens

<400> 110

atggagctgc ctgctgtgaa cctgaagggtg attctcctag gtcactggct gctgacaacc 60
 tggggctgca ttgtattctc aggtcctat gcctgggcca acttcaccat cctggccttg 120
 ggcggtgtgg ctgtggtcga gcgggactcc atcgacgcca taagcatgtt tctgggtggc 180
 ttgctggcca ccatcttctt ggacatcgtg cacatcagca tcttctaccc gcgggtcagc 240
 ctcacggaca cgggcccgtt tggcggtggc atggccatcc tcagcttgct gctcaagccg 300
 ctctcctgct gcttcgtota ccacatgtac cgggagcgcg ggggtgagct cctggtccac 360
 actggtttcc ttgggtcttc tcaggaccgt agtgcctacc agacgattga ctcagcagag 420
 gcgcccgcag atccctttgc agtcccagag ggcaggagtc aagatgcccg aggggtac 477

<210> 111

<211> 3438

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (121)...(1032)

<400> 111

gcctacgacg cctccgctag agcccgcggg gctgcgccga ctctgctct ggaggggttg 60
 cgggtacctg atggccacag agggctctag gaggccgagc gtgtaagcgg ggtgggcgcc 120
 atg gag gca gag cag cgg ccg gcg gcg ggg gcc agc gaa ggg gcg acc 168
 Met Glu Ala Glu Gln Arg Pro Ala Ala Gly Ala Ser Glu Gly Ala Thr
 1 5 10 15
 cct gga ctg gag gcg gtg cct ccc gtt gct ccc ccg cct gcg acc gcg 216
 Pro Gly Leu Glu Ala Val Pro Pro Val Ala Pro Pro Pro Ala Thr Ala

170/233

20	25	30	
gcc tca ggt ccg atc ccc aaa tot ggg cct gag cct aag agg agg cac			264
Ala Ser Gly Pro Ile Pro Lys Ser Gly Pro Glu Pro Lys Arg Arg His			
35	40	45	
ctt ggg acg ctg ctc cag cct acg gtc aac aag ttc tcc ctt cgg gtg			312
Leu Gly Thr Leu Leu Gln Pro Thr Val Asn Lys Phe Ser Leu Arg Val			
50	55	60	
ttc ggc agc cac aaa gca gtg gaa atc gag cag gag cgg gtg aag tca			360
Phe Gly Ser His Lys Ala Val Glu Ile Glu Gln Glu Arg Val Lys Ser			
65	70	75	80
gcg ggg gcc tgg atc atc cac ccc tac agc gac ttc cgg ttt tac tgg			408
Ala Gly Ala Trp Ile Ile His Pro Tyr Ser Asp Phe Arg Phe Tyr Trp			
85	90	95	
gac ctg atc atg ctg ctg ctg atg gtg ggg aac ctc atc gtc ctg cct			456
Asp Leu Ile Met Leu Leu Leu Met Val Gly Asn Leu Ile Val Leu Pro			
100	105	110	
gtg ggc atc acc ttc ttc aag gag gag aac tcc ccg cct tgg atc gtc			504
Val Gly Ile Thr Phe Phe Lys Glu Glu Asn Ser Pro Pro Trp Ile Val			
115	120	125	
ttc aac gta ttg tct gat act ttc ttc cta ctg gat ctg gtg ctc aac			552
Phe Asn Val Leu Ser Asp Thr Phe Phe Leu Leu Asp Leu Val Leu Asn			
130	135	140	
ttc cga acg ggc atc gtg gtg gag gag ggt gct gag atc ctg ctg gca			600
Phe Arg Thr Gly Ile Val Val Glu Glu Gly Ala Glu Ile Leu Leu Ala			
145	150	155	160
ccg cgg gcc atc cgc acg cgc tac ctg cgc acc tgg ttc ctg gtt gac			648
Pro Arg Ala Ile Arg Thr Arg Tyr Leu Arg Thr Trp Phe Leu Val Asp			
165	170	175	
ctc atc tct tct atc cct gtg gat tac atc ttc cta gtg gtg gag ctg			696
Leu Ile Ser Ser Ile Pro Val Asp Tyr Ile Phe Leu Val Val Glu Leu			
180	185	190	
gag cca cgg ttg gac gct gag gtc tac aaa acg gca cgg gcc cta cgc			744
Glu Pro Arg Leu Asp Ala Glu Val Tyr Lys Thr Ala Arg Ala Leu Arg			
195	200	205	
atc gtt cgc ttc acc aag atc cta agc ctg ctg agg ctg ctc cgc ctc			792

171/233

Ile Val Arg Phe Thr Lys Ile Leu Ser Leu Leu Arg Leu Leu Arg Leu
 210 215 220
 tcc cgc ctc atc cgc tac ata cac cag tgg gag gag atc ttt cac atg 840
 Ser Arg Leu Ile Arg Tyr Ile His Gln Trp Glu Glu Ile Phe His Met
 225 230 235 240
 acc tat gac ctg gcc agt gct gtg gtt cgc atc ttc aac ctc att ggg 888
 Thr Tyr Asp Leu Ala Ser Ala Val Val Arg Ile Phe Asn Leu Ile Gly
 245 250 255
 atg atg ctg ctg cta tgt cac tgg gat ggc tgt ctg cag ttc ctg gtg 936
 Met Met Leu Leu Leu Cys His Trp Asp Gly Cys Leu Gln Phe Leu Val
 260 265 270
 ccc atg ctg cag gac ttc cct ccc gac tgc tgg gtc tcc atc aac cac 984
 Pro Met Leu Gln Asp Phe Pro Pro Asp Cys Trp Val Ser Ile Asn His
 275 280 285
 atg gtg gtg aga agt ccc cac age tct gcc ttt cct ggg cct tct t 1030
 Met Val Val Arg Ser Pro His Ser Ser Ala Phe Pro Gly Pro Ser
 290 295 300
 agggctcttc tgcctgagta gcagggatgg ccacagggag caggaggtgg gagatgatca 1090
 caacagaaaa taggagcgag gaggtgggga ggagggagga aaggggaagg agaccagaa 1150
 gaagtgotcg tgtgttgag ggagcaggca aaggaagggg acctaccgg aagctgagggc 1210
 cccaagtgtg caatagagga cctttttgcc tcagggcccc ccagaaccaa acttaagtgc 1270
 ctgccaggag gaaggcctgc agtagaaggg gcagacagaa agaccaaaga aggaaaaggg 1330
 gcaggcagag aatgaggctc cgagggggccc atgccagct ctgcaatata ctctgccct 1390
 cagaaccact cgtggggccg ccagtattcc catgccctgt tcaaggccat gagccacatg 1450
 ctgtgcattg gctatgggca gcaggcacct gtaggcatgc ccgacgtctg gctcaccatg 1510
 ctcagcatga tcgtaggtgc cacatgttac gccatgttca tcggccatgc cacggcactc 1570
 atccagtccc tggactcttc cgggcgtcag taccaggaga agtacaagca ggtggagcag 1630
 tacatgtcct tccacaagct gccagcagac acgcggcagc gcatccacga gtactatgag 1690
 caccgtacc agggcaagat gttcgatgag gaaagcatcc tgggcgagct gagcgagccg 1750
 cttecgagag agatcattaa cttcacctgt cggggcctgg tggeccacat gccgtgttt 1810
 gcccatgccg accccagctt cgtcactgca gttctacca agctgcgctt tgaggtcttc 1870
 cagccggggg atctcgtggt gcgtgagggc tccgtgggga ggaagatgta cttcatccag 1930
 catgggctgc tcagtgtgct ggcgcgggc gcccgggaca cagccctcac cgatggatcc 1990
 tactttgggg agatctgcct gctaactagg ggccggcgca cagccagtgt tcgggctgac 2050
 acctactgcc gcctttactc actcagcgtg gaccatttca atgctgtgct tgaggagttc 2110

172/233

```

cccatgatgc gccgggcctt tgagactgtg gccatggatc ggctgctccg catcggcaag 2170
aagaattcca tactgcagcg gaagcgctcc gagccaagtc caggcagcag tgggtggcatc 2230
atggagcagc acttgggtgca acatgacaga gacatggctc ggggtgttcg gggtcggggc 2290
ccgagcacag gagctcagct tagtggaaaag ccagtaactgt gggagccact ggtacatgcg 2350
ccccttcagg cagctgctgt gacctccaat gtggccattg ccctgactca tcagcggggc 2410
cctctgcccc totcccctga ctctccagcc accctccttg ctgctctgc ttggcgtca 2470
gcaggctctc cagcttcccc gctgggtgcc gtccgagctg gcccatgggc atccacctcc 2530
cgcttgcctg ccccacctgc ccgaacctg cagccagcc tatccggggc agggcgctcc 2590
caggtctccc tgetgggtcc ccctccagga ggaggtggac ggcggctagg acctcggggc 2650
cgccccactc cagctccca accctctctg cctcagcggg caacaggcga tggctctcct 2710
gggcgtaagg gatcaggaag tgagcggtg cctccctcag ggctcctggc caaacctcca 2770
aggacagccc agccccccag gccaccagtg cctgagccag ccacaccccg gggctctccag 2830
ctttctgcca acatgtaaaa cctttgagta catccagcct tagttcttgg ggtgcagtag 2890
tatgtaccca agggcagatg cctcttgggg aaggccatgg ggacctgaaa cattgcccc 2950
tggaatgtc gacctgtgc ggacattccg catactgcca tgaagcggc ctctgtgtcc 3010
tcagctcaag aatcctgtag cttgtcccat cataatccat tcacccgttc atcatgtgta 3070
ctgagcagct accatgttca aggtaaggag acaggaggag taggaggagg cagggcctct 3130
ccatgccagc ctctgtgtgc cttgccccaa ccatcagcg caatacttga acctctccc 3190
aggtaggggc aggaggagcc acatgagaga gggagaagga ccgcgtttac ctttagagtt 3250
ttgttttgtt ttttcctct gagtttctg ttggtgcagg aataaggga aggcccaagg 3310
tatccaagcc tggggaaggg caggccagcc agcacctctg ccttctcagg gacaagagta 3370
gtcctttacc accctcactc tgcctgtccc ctctcctact ctacagcatt aaagactgtg 3420
ggaccagg 3438

```

<210> 112

<211> 1144

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (56)...(907)

<400> 112

```

caaggatctg gaacctgag cctcgaagcg gaggatccct gtgtcccagc cgggc 55
atg gcc gac ccc cac cag ctt ttc gat gac aca agt tca gcc cag agc 103
Met Ala Asp Pro His Gln Leu Phe Asp Asp Thr Ser Ser Ala Gln Ser

```


173/233

1	5	10	15	
cgg ggc tat ggg gcc cag cgg gca cct ggt ggc ctg agt tat cct gca	151			
Arg Gly Tyr Gly Ala Gln Arg Ala Pro Gly Gly Leu Ser Tyr Pro Ala				
20	25	30		
gcc tct ccc acg ccc cat gca gcc ttc ctg gct gac ccg gtg tcc aac	199			
Ala Ser Pro Thr Pro His Ala Ala Phe Leu Ala Asp Pro Val Ser Asn				
35	40	45		
atg gcc atg gcc tat ggg agc agc ctg gcc gcg cag ggc aag gag ctg	247			
Met Ala Met Ala Tyr Gly Ser Ser Leu Ala Ala Gln Gly Lys Glu Leu				
50	55	60		
gtg gat aag aac atc gac cgc ttc atc ccc atc acc aag ctc aag tat	295			
Val Asp Lys Asn Ile Asp Arg Phe Ile Pro Ile Thr Lys Leu Lys Tyr				
65	70	75	80	
tac ttt gct gtg gac acc atg tat gtg ggc aga aag ctg ggc ctg ctg	343			
Tyr Phe Ala Val Asp Thr Met Tyr Val Gly Arg Lys Leu Gly Leu Leu				
85	90	95		
ttc ttc ccc tac cta cac cag gac tgg gaa gtg cag tac caa cag gac	391			
Phe Phe Pro Tyr Leu His Gln Asp Trp Glu Val Gln Tyr Gln Gln Asp				
100	105	110		
acc ccg gtg gcc ccc cgc ttt gac gtc aat gcc ccg gac ctc tac att	439			
Thr Pro Val Ala Pro Arg Phe Asp Val Asn Ala Pro Asp Leu Tyr Ile				
115	120	125		
cca gca atg gct ttc atc acc tac gtt ttg gtg gct ggt ctt gcg ctg	487			
Pro Ala Met Ala Phe Ile Thr Tyr Val Leu Val Ala Gly Leu Ala Leu				
130	135	140		
ggg acc cag gat agg ttc tcc cca gac ctc ctg ggg ctg caa gcg agc	535			
Gly Thr Gln Asp Arg Phe Ser Pro Asp Leu Leu Gly Leu Gln Ala Ser				
145	150	155	160	
tca gcc ctg gcc tgg ctg acc ctg gag gtg ctg gcc atc ctg ctc agc	583			
Ser Ala Leu Ala Trp Leu Thr Leu Glu Val Leu Ala Ile Leu Leu Ser				
165	170	175		
ctc tat ctg gtc act gtc aac acc gac ctc acc acc atc gac ctg gtg	631			
Leu Tyr Leu Val Thr Val Asn Thr Asp Leu Thr Thr Ile Asp Leu Val				
180	185	190		
gcc ttc ttg ggc tac aaa tat gtc ggg atg att ggc ggg gtc ctc atg	679			

174/233

Ala Phe Leu Gly Tyr Lys Tyr Val Gly Met Ile Gly Gly Val Leu Met	
195	200 205
ggc ctg ctc ttc ggg aag att ggc tac tac ctg gtg ctg ggc tgg tgc	727
Gly Leu Leu Phe Gly Lys Ile Gly Tyr Tyr Leu Val Leu Gly Trp Cys	
210	215 220
tgc gta gcc atc ttt gtg ttc atg atc cgg acg ctg cgg ctg aag atc	775
Cys Val Ala Ile Phe Val Phe Met Ile Arg Thr Leu Arg Leu Lys Ile	
225	230 235 240
ttg gca gac gca gca gct gag ggg gtc cgg gtg cgt ggg gcc cgg aac	823
Leu Ala Asp Ala Ala Ala Glu Gly Val Pro Val Arg Gly Ala Arg Asn	
245	250 255
cag ctg cgc atg tac ctg acc atg gcg gtg gcg gcg cag cct atg	871
Gln Leu Arg Met Tyr Leu Thr Met Ala Val Ala Ala Ala Gln Pro Met	
260	265 270
ctc atg tac tgg ctc acc ttc cac ctg gtg cgg tgagcgcgcc cgctga	920
Leu Met Tyr Trp Leu Thr Phe His Leu Val Arg	
275	280
acctcccgcg gctgctgctg ctgctggggg ccactgtggc cgcggaactc atctcctgcc	980
tgcaggcccc aaggctcacc ctgtctggcc acaggcacgg cctccatccc atgtcccgcc	1040
cagccccgcc cccaacccaa ggtgctgaga gatctccagc tgcacaggcc accgccccag	1100
ggcgtggcgg ctgttacaga aacaataaac cctgatgggc atgg	1144
<210> 113	
<211> 2339	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> (253)...(1719)	
<400> 113	
ctttactcag ggcacagagg gtctctgcgg ccgtagcggc cggggctgcg gtageccaatt	60
tagatttggg caaggacttt agattcgggc tctgtttgt ttccgccgtc ctgcttctg	120
ccgaggctgg ccaggcagc cgcgcttcga aggacggc cgggagctgc ggagcatgcg	180
tggagtggca gtgctaacgg ctggtgtctc gcaactgttg cctgtgaagg tacgtgaagc	240
tgaagcctg ga atg gct gga aag ggg tca tca ggc agg cgg ccc ctg	288

175/233

Met Ala Gly Lys Gly Ser Ser Gly Arg Arg Pro Leu

1 5 10

ctg ctg ggg ctg ctg gtg gcc gta gcc act gtc cac ctg gtc atc tgt 336
 Leu Leu Gly Leu Leu Val Ala Val Ala Thr Val His Leu Val Ile Cys

15 20 25

ccc tac acc aaa gtg gag gag agc ttc aac ctg cag gcc aca cat gac 384
 Pro Tyr Thr Lys Val Glu Glu Ser Phe Asn Leu Gln Ala Thr His Asp

30 35 40

ctg ctc tac cac tgg caa gac ctg gag cag tac gac cat ctt gag ttc 432
 Leu Leu Tyr His Trp Gln Asp Leu Glu Gln Tyr Asp His Leu Glu Phe

45 50 55 60

ccc gga gtc gtc ccc agg acg ttc ctc ggg cca gtg gtg atc gca gtg 480
 Pro Gly Val Val Pro Arg Thr Phe Leu Gly Pro Val Val Ile Ala Val

65 70 75

ttc tcc agc ccc gcg gtt tac gtg ctt tcg ctg tta gaa atg tcc aag 528
 Phe Ser Ser Pro Ala Val Tyr Val Leu Ser Leu Leu Glu Met Ser Lys

80 85 90

ttt tac tct cag cta ata gtt aga gga gtg ctt gga ctc ggc gtg att 576
 Phe Tyr Ser Gln Leu Ile Val Arg Gly Val Leu Gly Leu Gly Val Ile

95 100 105

ttt gga ctc tgg acg tta caa aag gaa gtg aga cgg cac ttc ggg gcc 624
 Phe Gly Leu Trp Thr Leu Gln Lys Glu Val Arg Arg His Phe Gly Ala

110 115 120

atg gtg gcc acc atg ttc tgc tgg gtg acg gcc atg cag ttc cac ctg 672
 Met Val Ala Thr Met Phe Cys Trp Val Thr Ala Met Gln Phe His Leu

125 130 135 140

atg ttc tac tgc acg cgg aca ctg ccc aat gtg ctg gcc ctg cct gta 720
 Met Phe Tyr Cys Thr Arg Thr Leu Pro Asn Val Leu Ala Leu Pro Val

145 150 155

gtc ctg ctg gcc ctc gcg gcc tgg ctg cgg cac gag tgg gcc cgc ttc 768
 Val Leu Leu Ala Leu Ala Ala Trp Leu Arg His Glu Trp Ala Arg Phe

160 165 170

atc tgg ctg tca gcc ttc gcc atc atc gtg ttc agg gtg gag ctg tgc 816
 Ile Trp Leu Ser Ala Phe Ala Ile Ile Val Phe Arg Val Glu Leu Cys

175 180 185

176/233

ctg ttc ctg ggc ctc ctg ctg ctg ctg gcc ttg ggc aac cga aag gtt	864
Leu Phe Leu Gly Leu Leu Leu Leu Leu Ala Leu Gly Asn Arg Lys Val	
190 195 200	
tct gta gtc aga gcc ctt cgc cac gcc gtc ccg gca ggg atc ctc tgt	912
Ser Val Val Arg Ala Leu Arg His Ala Val Pro Ala Gly Ile Leu Cys	
205 210 215 220	
tta gga ctg acg gtt gct gtg gac tct tat ttt tgg cgg cag ctc act	960
Leu Gly Leu Thr Val Ala Val Asp Ser Tyr Phe Trp Arg Gln Leu Thr	
225 230 235	
tgg ccg gaa gga aag gtg ctt tgg tac aac act gtc ctg aac aaa agc	1008
Trp Pro Glu Gly Lys Val Leu Trp Tyr Asn Thr Val Leu Asn Lys Ser	
240 245 250	
tcc aac tgg ggg acc tcc ccg ctg ctg tgg tac ttc tac tca gcc ctg	1056
Ser Asn Trp Gly Thr Ser Pro Leu Leu Trp Tyr Phe Tyr Ser Ala Leu	
255 260 265	
ccc cgc ggc ctg ggc tgc agc ctg ctc ttc atc ccc ctg ggc ttg gta	1104
Pro Arg Gly Leu Gly Cys Ser Leu Leu Phe Ile Pro Leu Gly Leu Val	
270 275 280	
gac aga agg acg cac gcg ccg acg gtg ctg gca ctg ggc ttc atg gca	1152
Asp Arg Arg Thr His Ala Pro Thr Val Leu Ala Leu Gly Phe Met Ala	
285 290 295 300	
ctc tac tcc ctc ctg cca cac aag gag cta cgc ttc atc atc tat gcc	1200
Leu Tyr Ser Leu Leu Pro His Lys Glu Leu Arg Phe Ile Ile Tyr Ala	
305 310 315	
ttc ccc atg ctc aac atc acg gct gcc aga ggc tgc tcc tac ctg ctg	1248
Phe Pro Met Leu Asn Ile Thr Ala Ala Arg Gly Cys Ser Tyr Leu Leu	
320 325 330	
aat aac tat aaa aag tct tgg ctg tac aaa gca ggg tct ctg ctt gtg	1296
Asn Asn Tyr Lys Lys Ser Trp Leu Tyr Lys Ala Gly Ser Leu Leu Val	
335 340 345	
atc gga cac ctc gtg gtg aat gcc gcc tac tca gcc acg gcc ctg tat	1344
Ile Gly His Leu Val Val Asn Ala Ala Tyr Ser Ala Thr Ala Leu Tyr	
350 355 360	
gtg tcc cat ttc aac tac cca ggt ggc gtc gca atg cag agg ctg cac	1392
Val Ser His Phe Asn Tyr Pro Gly Gly Val Ala Met Gln Arg Leu His	

177/233

365	370	375	380	
cag ctg gtg ccc ccc cag aca gac gtc ctt ctg cac att gac gtg gca				1440
Gln Leu Val Pro Pro Gln Thr Asp Val Leu Leu His Ile Asp Val Ala				
385	390	395		
gcc gcc cag aca ggt gtg tct cgg ttt ctc caa gtc aac agc gcc tgg				1488
Ala Ala Gln Thr Gly Val Ser Arg Phe Leu Gln Val Asn Ser Ala Trp				
400	405	410		
agg tac gac aag agg gag gat gtg cag ccg ggg aca ggc atg ctg gca				1536
Arg Tyr Asp Lys Arg Glu Asp Val Gln Pro Gly Thr Gly Met Leu Ala				
415	420	425		
tac aca cac atc ctc atg gag gcg gcc cct ggg ctc ctg gcc ctc tac				1584
Tyr Thr His Ile Leu Met Glu Ala Ala Pro Gly Leu Leu Ala Leu Tyr				
430	435	440		
agg gac aca cac cgg gtc ctg gcc agc gtc gtg ggg acc aca ggt gtg				1632
Arg Asp Thr His Arg Val Leu Ala Ser Val Val Gly Thr Thr Gly Val				
445	450	455	460	
agt ctg aac ctg acc caa ctg ccc ccc ttc aac gtc cac ctg cag aca				1680
Ser Leu Asn Leu Thr Gln Leu Pro Pro Phe Asn Val His Leu Gln Thr				
465	470	475		
aag ctg gtg ctt ctg gag agg ctc ccc cgg ccg tcc tgagggggac cagg				1730
Lys Leu Val Leu Leu Glu Arg Leu Pro Arg Pro Ser				
480	485			
cagccctcag cagccacagg ccttcaggga gctgttatca ctaccagttt ctggcacaat				1790
tccagcaciaa ttatgacaat tcagagaagc aagtcaaagg actggggcacc tgccctctgac				1850
agacaccaga ccagggtccag ggcctcctcc acagcctcag ctggggctct cagcaccaaa				1910
gaacgagggg cccagggtctt gttggcacc cgggagccac tgcccagggt gatggtggcc				1970
agctcagggc ttctgctggg tgactgtcgc ccagaccagg tgccattcat gactaatcag				2030
gagcagcggg ctcaccagg cactgtctg ccaggaggcc acgtgtgtcc tgcccaccca				2090
gggggagctg ttttttgga gcacccacg cttgtgtgcc gagggcctct tggggcacct				2150
aagacagcac cccctctcag gggagaccat ggtggccccg gccgcacccc cccaccctgg				2210
tgccaccact gcaacttttg tattcacagg catcccatct ccatcacaga taaaatctta				2270
ggagataaac acattcaaaa aggaatgaga taaaaagaat aaggcaataa atgttgattg				2330
gaacctctc				2339

<210> 114

178/233

<211> 1756

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (102)...(650)

<400> 114

```

gtgtgcgctg cctccttcc gcacagcccg ggtttccgct tccctccggg cgcgagaaga      60
ggggagccag gccgagcccc ggccctaccg ccgcgcgcgc c atg tgg ccc cca      113
                                     Met Trp Pro Pro
                                     1

gac ccc gac ccc gac ccg gac ccc gag cct gcc ggc ggc tcc cgt ccc      161
Asp Pro Asp Pro Asp Pro Asp Pro Glu Pro Ala Gly Gly Ser Arg Pro
   5                10                15                20

ggc ccc gcg gtc ccc ggg ctc cgc gcc ctg ctg ccg gcg cgg gct ttc      209
Gly Pro Ala Val Pro Gly Leu Arg Ala Leu Leu Pro Ala Arg Ala Phe
                25                30                35

ctc tgc tct ctc aaa ggc cgc ctc ctg ctg gcc gag tcg ggt ctc tca      257
Leu Cys Ser Leu Lys Gly Arg Leu Leu Leu Ala Glu Ser Gly Leu Ser
                40                45                50

ttc atc act ttt atc tgc tat gtg gcg tcc tca gca tct gcc ttc ctc      305
Phe Ile Thr Phe Ile Cys Tyr Val Ala Ser Ser Ala Ser Ala Phe Leu
                55                60                65

aca gcg cct ctg ctg gag ttc ctg ctg gcc ttg tac ttc ctc ttt gct      353
Thr Ala Pro Leu Leu Glu Phe Leu Leu Ala Leu Tyr Phe Leu Phe Ala
                70                75                80

gat gcc atg cag ctg aat gac aag tgg cag ggc ttg tgc tgg ccc atg      401
Asp Ala Met Gln Leu Asn Asp Lys Trp Gln Gly Leu Cys Trp Pro Met
                85                90                95                100

atg gac ttc ctg cgc tgt gtc acc gcg gcc ctc atc tac ttt gct atc      449
Met Asp Phe Leu Arg Cys Val Thr Ala Ala Leu Ile Tyr Phe Ala Ile
                105                110                115

tcc atc acg gcc atc gcc aag tac tcg gat ggg gct tcc aaa gcc gct      497
Ser Ile Thr Ala Ile Ala Lys Tyr Ser Asp Gly Ala Ser Lys Ala Ala
                120                125                130

```

179/233

ggg gtg ttt ggc ttc ttt gct acc atc gtg ttt gca act gat ttc tac 545
 Gly Val Phe Gly Phe Phe Ala Thr Ile Val Phe Ala Thr Asp Phe Tyr
 135 140 145
 ctg atc ttt aac gac gtg gcc aaa ttc ctc aaa caa ggg gac tct gca 593
 Leu Ile Phe Asn Asp Val Ala Lys Phe Leu Lys Gln Gly Asp Ser Ala
 150 155 160
 gat gag acc aca gcc cac aag aca gaa gaa gag aat tcc gac tcg gac 641
 Asp Glu Thr Thr Ala His Lys Thr Glu Glu Glu Asn Ser Asp Ser Asp
 165 170 175 180
 tct gac tgaaggcctg gcgggtgcct tggcaacctg agccacacag gcc 690
 Ser Asp

tccacccctg cgcctcacag gggtogetgg cgttggagcg gaggcctgga cttctgagtt 750
 gcagaggggg ctgcggacac agcaggcccc ctacagcctc aggttctgcc tgagcccagc 810
 ctaccaggct tgcccctcag ctcagcactg ttgaccacgc tgcgtatgag ggcattcttg 870
 gtatcccact ccttctcccc atttctgtcc cacaggcctt cagcccttta acgtctctgc 930
 caaaaaccag cacaaggaga caaagcagag ccttgtctgt atctgggcag caggtgttcc 990
 atgtgtctag gtggcggggg tcgggggtct tctgtttcac taacaggaac aaagacagaa 1050
 accatgacag ggctgccccg ccaggccccg gtgggtttgt ctgcacttgg tgctcctgcc 1110
 cacaccagcc actttggtga caatgacctc tccaagaatc tttggttcaa ggagcaccag 1170
 ttccctcttc attcttgaag cagggagaaa ttgaccttg ccttgtcgcc caggaagtgg 1230
 ggctcggcac ccataactaa cacctcccac ccttggaac catgtcttct gggggtgaga 1290
 tgaccattct ggggtctaaga ctgtttcaaa gaagagctca tagactgact ggtccagaag 1350
 acagagggta caacagtggc atcacagtga cagtgtcatg gggagotggg cgggcccagc 1410
 caaacctctc ttcttcctag agcccagcca gcaggcagga gttcctggac cctcaggaca 1470
 gtgaacttcc agacctcagg gcaggcttat gggccactgc aggagatgag accagccttc 1530
 tgtgttcacc taacgattta tactgtgtat ctgtctttga tggaattttg taacttttta 1590
 tattttttta tgcaaaagca gcttcttaac agatggcatt ttctgtgact ctaggcctca 1650
 caaaagagcc agagttctgg acccatgttt ggagcatttg tagccttatt ctcttgctg 1710
 tgaatctctt accctgaaaa aaagccataa tgaattaagc caaaag 1756

<210> 115

<211> 1418

<212> DNA

<213> Homo sapiens

180/233

<220>

<221> CDS

<222> (149)...(703)

<400> 115

```

attggtccta gcgggggggc gggggcgac accggcgcg ggccggagca gcgcggtca      60
ggctgcggga aagcgggtgc cgtgcagcgg ggtgggtgcc ctggtccgcg ggcgagctcg    120
agcagccaac ccggggcgcg tcggggcc atg gac ggc ctg agg cag cgc gtg      172
Met Asp Gly Leu Arg Gln Arg Val
      1              5
gag cac ttc ctg gag caa agg aac ctg gtc acc gaa gtg ctg ggg gcg      220
Glu His Phe Leu Glu Gln Arg Asn Leu Val Thr Glu Val Leu Gly Ala
      10              15              20
ctg gag gcc aag acc ggg gtg gag aag cgg tat ctg gct gca gga gcc      268
Leu Glu Ala Lys Thr Gly Val Glu Lys Arg Tyr Leu Ala Ala Gly Ala
      25              30              35              40
gtc act ctg cta agc ctg tat ctg ctg ttc ggc tac gga gcg tct ctg      316
Val Thr Leu Leu Ser Leu Tyr Leu Leu Phe Gly Tyr Gly Ala Ser Leu
      45              50              55
ctg tgc aat ctc atc gga ttt gtg tac ccc gca tat gcc tca atc aaa      364
Leu Cys Asn Leu Ile Gly Phe Val Tyr Pro Ala Tyr Ala Ser Ile Lys
      60              65              70
gct atc gag agc cca agc aag gac gac gac act gtg tgg ctc acc tac      412
Ala Ile Glu Ser Pro Ser Lys Asp Asp Asp Thr Val Trp Leu Thr Tyr
      75              80              85
tgg gtg gtg tac gcc ctg ttt ggg ctg gcc gag ttc ttc agc gat cta      460
Trp Val Val Tyr Ala Leu Phe Gly Leu Ala Glu Phe Phe Ser Asp Leu
      90              95              100
ctc ctg tcc tgg ttc cct ttc tac tac gtg ggc aag tgc gcc ttc ctg      508
Leu Leu Ser Trp Phe Pro Phe Tyr Tyr Val Gly Lys Cys Ala Phe Leu
      105              110              115              120
ttg ttc tgc atg gct ccc agg ccc tgg aac ggg gct ctc atg ctg tat      556
Leu Phe Cys Met Ala Pro Arg Pro Trp Asn Gly Ala Leu Met Leu Tyr
      125              130              135
cag cgc gtc gtg cgt ccg ctg ttc cta agg cac cac ggg gcc gta gac      604
Gln Arg Val Val Arg Pro Leu Phe Leu Arg His His Gly Ala Val Asp

```


181/233

140	145	150	
aga atc atg aac gac ctc agc ggg cga gcc ctg gac gcg gcg gcc gga			652
Arg Ile Met Asn Asp Leu Ser Gly Arg Ala Leu Asp Ala Ala Ala Gly			
155	160	165	
ata acc agg aac gtc aag cca agc cag acc ccg cag ccg aag gac aag			700
Ile Thr Arg Asn Val Lys Pro Ser Gln Thr Pro Gln Pro Lys Asp Lys			
170	175	180	
tgaagcagcc ccctgagcct cacaaggacc tcctggctgg tgaggagggg gccgcgccag			760
gtccccaggc ctccacagag tcttcagcgc atcccccaac agcagcccct gccagtcct			820
cgggtccagg caaggccctg ggggtctcct taaatgccac ctcgggcaag tccagtecc			880
agtcctcggc cacccccagc tctggatccc agggccagct gccctctggc tctggctgtg			940
gtccccgct gtccggcagg gcccagggcc agcgtcgggc acagggcagc tccactgg			1000
ctcggaaca caccagccg cctggtactt cctccggccc ctcccagtea gccctccgt			1060
cctcggggccc cctgcagcca cccaacgtca cctccagccc ggtctcacc atggtccagt			1120
ctcccagcag cagcaacatc cccacgcagc ccccagcaa gtcctctggc aagccggagg			1180
acgcagcccc caagaccagc ggacagcgcc agaaggaatc gtcgaaacag cctgccagca			1240
gcgcctcagt gcccgagctg gtcccctgcc attccgggac ctctctggag tacacttcgg			1300
agtccaccac cgagatcacc tgcagctggc cacaccacag gccccctgc ctgcagcact			1360
actggtgcct gaaacacctg gcctgctagg aggtccaat aaagctaacc cggaccag			1418

<210> 116

<211> 1211

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (133)...(555)

<400> 116

gaaaatggct caggtggact ccgggctgga gctgtcctgg gggagcttgt ttgcggcagc	60
ggctgctgct gccactgctg tgetgggggc ccggtcgcca ggcaaaaagc cctcccacgt	120
ttgaggggag tc atg agc cgt ttc ctg aat gtg tta aga agt tgg ctg	168

Met Ser Arg Phe Leu Asn Val Leu Arg Ser Trp Leu

1

5

10

gtt atg gtg tcc atc ata gcc atg ggg aac acg ctg cag agc ttc cga	216
Val Met Val Ser Ile Ile Ala Met Gly Asn Thr Leu Gln Ser Phe Arg	

182/233

15	20	25	
gac cac act ttt ctc tat gaa aag ctc tac act ggc aag cca aac ctt			264
Asp His Thr Phe Leu Tyr Glu Lys Leu Tyr Thr Gly Lys Pro Asn Leu			
30	35	40	
gtg aat ggc ctc caa gct cgg acc ttt ggg atc tgg acg ctg ctc tca			312
Val Asn Gly Leu Gln Ala Arg Thr Phe Gly Ile Trp Thr Leu Leu Ser			
45	50	55	60
tca gtg att cgc tgc ctc tgt gcc att gac att cac aac aag acg ctc			360
Ser Val Ile Arg Cys Leu Cys Ala Ile Asp Ile His Asn Lys Thr Leu			
65	70	75	
tat cac atc aca ctc tgg acc ttc ctc ctt gcc ctg ggg cat ttc ctc			408
Tyr His Ile Thr Leu Trp Thr Phe Leu Leu Ala Leu Gly His Phe Leu			
80	85	90	
tct gag ttg ttt gtc tat gga act gca gct ccc acg att ggc gtc ctg			456
Ser Glu Leu Phe Val Tyr Gly Thr Ala Ala Pro Thr Ile Gly Val Leu			
95	100	105	
gca ccc ctg atg gtg gca agt ttc tcc atc ctg ggt atg ctg gtc ggg			504
Ala Pro Leu Met Val Ala Ser Phe Ser Ile Leu Gly Met Leu Val Gly			
110	115	120	
ctc cgg tat cta gaa gta gaa cca gta tcc aga cag aag aag aga aac			552
Leu Arg Tyr Leu Glu Val Glu Pro Val Ser Arg Gln Lys Lys Arg Asn			
125	130	135	140
tgaggcca gcattatcac ctccaggact ttctcgtttt ccaccttggc catctttctt			610
cttcgtcgtc tctcctcttt aatttctttt ctattccatc atctgccott ttattoactt			670
ttagcctctt tttttaattt ttaaaattta aagatatgca tactgaaaag tatataacat			730
gtacgtacaa tttaaagaat aattttaaag tgaatactac gtaactccat ccaagtcaag			790
aaattgccag cttctcggaa gccactgtg tctccttccc ctacctgcaa cctottccag			850
gtcctctttt ccagccttcc cctttttccc ttttattttc atgccttgat ttgacttggt			910
tggtgggaac atgtgaacta tgaaacttaa acctgctgcc caccagagc agctgtgacc			970
aagggtgcc tcaaggggtt gtccacgcag gttgggtcc tetctgctgc tggacccaag			1030
actctgaacc ttccaagga caggcagttc ttctaagaag ggtcccttg tgtgtgagca			1090
agaccacagc tctccttcta tctacagatg catgagggtt ggaagagtct gggctgtttt			1150
tagaccttct ggctcagctgt atttgtgtaa caacttttgt aataaataga aaaacctct			1210
g			1211

183/233

<210> 117

<211> 1099

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (183)...(644)

<400> 117

```

gtatccgcgg ccgtagcagc cgggctggtc ctgctgcgag ccggcggccc ggagtggggc      60
ggcggcatgt accttcacaca ttgagtattc agaaagaagt gatctgaact ctgaccattc      120
tttatggata cattaagtca aatataagag tctgactact tgacacactg gctcgagcaa      180
ac atg aac gtt gga gtt gcc cac agt gaa gtg aat cca aat acc cgt      227
    Met Asn Val Gly Val Ala His Ser Glu Val Asn Pro Asn Thr Arg
      1             5             10             15
gtc atg aac agc cgg ggt atg tgg ctg aca tat gca ttg gga gtt ggc      275
Val Met Asn Ser Arg Gly Met Trp Leu Thr Tyr Ala Leu Gly Val Gly
      20             25             30
ttg ctt cat att gtc tta ctc agc att ccc ttc ttc agt gtt cct gtt      323
Leu Leu His Ile Val Leu Leu Ser Ile Pro Phe Phe Ser Val Pro Val
      35             40             45
gct tgg act tta aca aat att ata cat aat ctg ggg atg tac gta ttt      371
Ala Trp Thr Leu Thr Asn Ile Ile His Asn Leu Gly Met Tyr Val Phe
      50             55             60
ttg cat gca gtg aaa gga aca cct ttc gaa act cct gac cag ggt aaa      419
Leu His Ala Val Lys Gly Thr Pro Phe Glu Thr Pro Asp Gln Gly Lys
      65             70             75
gca agg ctc cta act cat tgg gaa caa ctg gac tat gga gta cag ttt      467
Ala Arg Leu Leu Thr His Trp Glu Gln Leu Asp Tyr Gly Val Gln Phe
      80             85             90             95
aca tct tca cgg aag ttt ttc aca att tct cca ata att cta tat ttt      515
Thr Ser Ser Arg Lys Phe Phe Thr Ile Ser Pro Ile Ile Leu Tyr Phe
      100             105             110
ctg gca agt ttc tat acg aag tat gat cca act cac ttc atc cta aac      563
Leu Ala Ser Phe Tyr Thr Lys Tyr Asp Pro Thr His Phe Ile Leu Asn
      115             120             125

```

184/233

aca gct tct ctc ctg agt gta cta att ccc aaa atg cca caa cta cat 611
 Thr Ala Ser Leu Leu Ser Val Leu Ile Pro Lys Met Pro Gln Leu His
 130 135 140
 ggt gtt cgg atc ttt gga att aat aag tat tgaaatgttt tgaaactga 660
 Gly Val Arg Ile Phe Gly Ile Asn Lys Tyr
 145 150
 aaaaaaattt tacagctact gaattttotta taaggaagga gtggttagta aactgcactg 720
 tttctctgat aatgtgaaat gagaagtatt tacattggag ggccaatggc tggctccttca 780
 agtgcgtgttt tgaagtgcag atttccatta aatgatgcct ctgtttaata cacctgggtac 840
 atttctgaag aggggcttta taagcaggct gggcaggccc agcttataag ttaaagggca 900
 tcacagtgcg ggtgtagtag ataaattcaa ggaaataaga gatttgtaag aaactaggac 960
 cagcttaact tataatgaat gggcattgtg ttaagaaaag aacatttcca gtcattcagc 1020
 tgtggttatt taaagcagac ttacatgtaa accggaatcc tctctataca agtttattaa 1080
 agattatttt tattaccgt 1099

<210> 118

<211> 3489

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (227)...(748)

<400> 118

gcgtgcattt ttctggagaa ctgcatgcat catgctctct ctgtgtgcat tttcctggac 60
 aaaagcccat agtgcctatc agattctcaa agggactcct gactccagaa agtttaaaaa 120
 ccattaggct taaggaagca catacctact ctgtactcca gggaccaggt gggaacagct 180
 gagtgcaggg agtggettct tctttcagac cctctcccgg agcccc atg gct gcc 235

Met Ala Ala

1

ttc ctg ata cag acc aag gac aac ccc atg aag gcc gtg ggt gtg ctg 283
 Phe Leu Ile Gln Thr Lys Asp Asn Pro Met Lys Ala Val Gly Val Leu
 5 10 15
 gcc ggc acc atg gcc acc gtc gtg gcc atc act gtc ctc atc tcc acc 331
 Ala Gly Thr Met Ala Thr Val Val Ala Ile Thr Val Leu Ile Ser Thr
 20 25 30 35

185/233

gcc acc ttc tgg cgc aac aag aag tct aac aag gtc ctg cca atg cgg	379
Ala Thr Phe Trp Arg Asn Lys Lys Ser Asn Lys Val Leu Pro Met Arg	
40 45 50	
cgg gtg ctc cgc aag cgg ccc agc cct gcg ccc cgc acc atc cgc att	427
Arg Val Leu Arg Lys Arg Pro Ser Pro Ala Pro Arg Thr Ile Arg Ile	
55 60 65	
gag tgg ctc aag tcc aag agc acc aaa gcc gct acc aag ttc atg ctc	475
Glu Trp Leu Lys Ser Lys Ser Thr Lys Ala Ala Thr Lys Phe Met Leu	
70 75 80	
aaa gag aaa cct ccc aat gag aac tgt aac aac aac agc cca gaa agc	523
Lys Glu Lys Pro Pro Asn Glu Asn Cys Asn Asn Asn Ser Pro Glu Ser	
85 90 95	
tct ctg ctc ccg aga gct ccg gct ctc cct cca cca ccc agc gtg gcg	571
Ser Leu Leu Pro Arg Ala Pro Ala Leu Pro Pro Pro Pro Ser Val Ala	
100 105 110 115	
ccc agc act ggc gca gcc cag tgg acc gtg cct act gtc tct ggc tct	619
Pro Ser Thr Gly Ala Ala Gln Trp Thr Val Pro Thr Val Ser Gly Ser	
120 125 130	
ctc act ccg cag ccg acc caa ccc ccg cca aaa ccc aaa act atg gga	667
Leu Thr Pro Gln Pro Thr Gln Pro Pro Pro Lys Pro Lys Thr Met Gly	
135 140 145	
agc ccc gtc cag tca act ctg atc tct gag ctc aag caa aag ttt gag	715
Ser Pro Val Gln Ser Thr Leu Ile Ser Glu Leu Lys Gln Lys Phe Glu	
150 155 160	
aag aag agt gtg cac aac aag gct tac ttc tagtgtatgc cctat	760
Lys Lys Ser Val His Asn Lys Ala Tyr Phe	
165 170	
gaccccccat ctttctctcg ccctgaccc ccaccacct gctgctcgga ctatgctccc	820
cttctctctgc tcttaaggt cactgacccc tgttttgac aatggtataa tccccactgt	880
cctcatctct accgccacct tctggcgcaa caagaagttg cgtcttgaca gggctctagt	940
cagggccttg ggcaagacat tgggctctag gatgcaattg gcaaatacgt ccccgttact	1000
caaatccttg gcaactactac aatgccctcc attcttcagg gctgagaatt gacgagaagc	1060
cagctcaccc atcccagacc tcacagtcctc tcagggttcta ctgggatctc atcatcatcc	1120
ttagtcaagc agcagggccc tggccacgtg gagcaaacct gactagaatc tggatcctga	1180
cgctgcagc tgagagcagg agcaggaaaa ggaggetcag cactgtctca ggctggaggt	1240

186/233

cagcgaacct	cgtgggctgt	aggaaagcaa	atgtaggtaa	ggggagagca	aggatgcaca	1300
gaaaacacac	tgactgtggg	actgtgccag	gatgcatttg	gaaagataga	gcattctgtc	1360
tgggcagaga	ctgtggaccc	tggtagcccc	acgtgggaca	gaggacacag	aggtggaaga	1420
ttgatcttgc	caagagttag	ggcagatgtc	tccagccagg	actgccctga	gccgcaaaat	1480
gtcaaagctg	gagctataga	ggtagcccta	aaggcaacta	gaagagcatc	agggctgtct	1540
tctgaggagc	tgccccacca	gccatccttg	aagagacaat	tcagggcagt	tgatgaatat	1600
cagggctgag	atgtggtgag	acttccgttt	ttatccagct	cttttgetca	catcgcgtaa	1660
ccttgggaaa	gctgtttaaa	gtcgtgtgatc	atcctcttcc	tcactctgtaa	atgaagaaaag	1720
taggccctgt	ctacctcaca	tgcaggtcta	gggtgaggat	tgaagaaaat	agtgggtgatg	1780
agggctttaa	ccaagtgcaa	agcggcatga	atgcaaagta	tttttctgca	gccaggttct	1840
gtgggtgcag	ctcttccaga	aagtattagg	agcctcacat	ctactctgcc	aagcgcccca	1900
gcaggcactg	tgttgggctt	aggggctacc	actggatgat	ggcattgccg	tgactcacac	1960
acctctactt	ctgtttcttc	ctcactccat	ccccgtacc	gtcctggcca	gctaccgtca	2020
gagagaacca	gagctccaag	tctttaattt	gccaagatga	agaaaatgag	ttctcaagga	2080
gggaatgctt	tgtttgaggc	cacacagcag	gttggtagca	aagatcttgt	ctagccaggg	2140
cagcccttat	cagcttgtga	caaccttccc	caggacagaa	gtcatacaag	gcctctgggg	2200
ttaatacaaa	taggttgtgc	cctgtcttaa	ggaacctgct	atcaggaaat	ctacatgtgt	2260
gcacagagag	agaaaagtag	aacagttctt	tgcatttggc	tctacttact	aacaacctct	2320
ctagaataca	ttggtgattt	catttaaaga	gattgtatgc	atttgtggct	ttcctgattt	2380
ctgagtctgt	gtttggaggt	gttactgaga	tgtgccagtg	tgagaatcc	ttgttggggt	2440
ttctacagtc	cccaacgtga	acagtattaa	gcaagaggtg	gactcgagca	atccaggagc	2500
ccagactgag	caaataagta	ctttccagcc	tgtgtttcag	gagaggactg	tgttggatca	2560
tgttggcct	ccacagggaa	tacagcatcc	ttacagcttg	catgcaatca	acctcttttg	2620
taaattggaaa	ataaagtctg	ttacccaaag	gccatgctga	tcccctgtct	cctgtcttca	2680
tttatgtttg	ctgacctgtg	gagaccagtc	tttctgacac	acagtgaagc	tcaacttgcc	2740
tcctggctgc	ttcagcaggt	ggatccattc	ttcgaccccc	agatgtgact	ctaaagaagg	2800
ctgaaaattt	ttgtccaaat	tgccatgcag	atatcttgaa	cagcaggaca	tttgcaggcc	2860
ttgtctactg	gactttttct	ccaaacagga	caagcccagg	cagggtgca	tggagaggaa	2920
tggaaacctg	agctagaatt	aattgcccac	tctcccaccc	taccagtga	gcccggaag	2980
ggcagggaatt	gggaggccta	gggtgggcat	gaaagcttgg	gaagcactgt	cgtctctcag	3040
acaggcgctc	taaagacctc	taggctggaa	gcttgggctt	gcaagtggat	ccgggaccga	3100
gggtggtctc	ttggacaacc	ccaggaaactt	ggaccaaggc	agagccaatc	ttgcaaactg	3160
gccatggatg	gggaagtgcc	cggtagccag	catgagccac	actaggaaaag	aggaggaggg	3220
tgcagccaaa	cttaaggcac	cggcaagtgt	tgtcagcact	ggaggagacc	ccgccagtgg	3280
ggtgaggcca	gccaaagtccc	tgtgttacga	atggtgggccc	aaggggctgt	ctgctaggtc	3340

187/233

cagtaggaca ggcagagctc caggctggca ccatggtagg cctccagga aagagctggg 3400
 aggcaggaat ggcacactgg gcaggcttgc ccattcctgg ccctgagaat ggagctgtag 3460
 cctcatggac aataaatgga tgtgacacc 3489

<210> 119

<211> 931

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (25)...(252)

<400> 119

ctgacggacg cttcgccgt aacg atg atc gga gac atc ctg ctg ttc ggg 51
 Met Ile Gly Asp Ile Leu Leu Phe Gly

1

5

acg ttg ctg atg aat gcc ggg gcg gtg ctg aac ttt aag ctg aaa aag 99
 Thr Leu Leu Met Asn Ala Gly Ala Val Leu Asn Phe Lys Leu Lys Lys

10

15

20

25

aag gac acg cag ggc ttt ggg gag gag tcc agg gag ccc agc aca ggt 147
 Lys Asp Thr Gln Gly Phe Gly Glu Glu Ser Arg Glu Pro Ser Thr Gly

30

35

40

gac aac atc cgg gaa ttc ttg ctg agc etc aga tac ttt cga atc ttc 195
 Asp Asn Ile Arg Glu Phe Leu Leu Ser Leu Arg Tyr Phe Arg Ile Phe

45

50

55

atc gcc ctg tgg aac atc ttc atg atg ttc tgc atg att gtg ctg ttc 243
 Ile Ala Leu Trp Asn Ile Phe Met Met Phe Cys Met Ile Val Leu Phe

60

65

70

ggc tct tgaatcccag cgatgaaacc aggaactcac tttcccggga tgccgagtct c 300
 Gly Ser

75

cattcctcca ttctgatga cttcaagaat gtttttgacc agaaaaccga caaccttccc 360
 agaaagtcca agctcgtggt ggggtgaaaa gtgttcgcca aggtgtgcat ggtttcccag 420
 ccacgtccct gttttcaaag atagtttcac tttggtctct gaattgaaat gctgtctact 480
 gaaaggggtt caggagcgtt tatgtaaggg gctgtgatga aattgcattc cccatagata 540
 aaagaaaaat catttctatc cagagatctg agcagaagga ttggttgtt agtttaacac 600

188/233

agccgtgttt ttggacattc agtggtactt gctgagtctg acagcctctg ggcccggcca 660
 gggggccctgt taacaaactg ctttcacatc ccaacagggt ctgcttgccc actcagtga 720
 gctgcgatta accctaaagg ctttaaggaa cggggccacct gtaacagaga caccagcctt 780
 cctgtataga cactaaattg ttagcaagag tgttgagcta gttcctggtg aagtgtttcc 840
 acagaagaca tgtggagcag ttgtggggat attaaggga actttcctct gccttgaccc 900
 ctttgttaaa taaaatgact ttgggagcca t 931

<210> 120

<211> 1123

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (68)...(547)

<400> 120

gtccccgag ttgggagcct aggagccccc cgcggctgcg gcgcaggtgc cctcggcctg 60
 agtcggg atg gag ctg cct gct gtg aac ctg aag gtg att ctc cta ggt 109
 Met Glu Leu Pro Ala Val Asn Leu Lys Val Ile Leu Leu Gly
 1 5 10
 cac tgg ctg ctg aca acc tgg ggc tgc att gta ttc tca ggc tcc tat 157
 His Trp Leu Leu Thr Thr Trp Gly Cys Ile Val Phe Ser Gly Ser Tyr
 15 20 25 30
 gcc tgg gcc aac ttc acc atc ctg gcc ttg ggc gtg tgg gct gtg gct 205
 Ala Trp Ala Asn Phe Thr Ile Leu Ala Leu Gly Val Trp Ala Val Ala
 35 40 45
 cag cgg gac tcc atc gac gcc ata agc atg ttt ctg ggt ggc ttg ctg 253
 Gln Arg Asp Ser Ile Asp Ala Ile Ser Met Phe Leu Gly Gly Leu Leu
 50 55 60
 gcc acc atc ttc ctg gac atc gtg cac atc agc atc ttc tac ccg cgg 301
 Ala Thr Ile Phe Leu Asp Ile Val His Ile Ser Ile Phe Tyr Pro Arg
 65 70 75
 gtc agc ctc acg gac acg ggc cgc ttt ggc gtg ggc atg gcc atc ctc 349
 Val Ser Leu Thr Asp Thr Gly Arg Phe Gly Val Gly Met Ala Ile Leu
 80 85 90
 agc ttg ctg ctc aag ccg ctc tcc tgc tgc ttc gtc tac cac atg tac 397

189/233

Ser Leu Leu Leu Lys Pro Leu Ser Cys Cys Phe Val Tyr His Met Tyr
 95 100 105 110
 cgg gag cgc ggg ggt gag ctc ctg gtc cac act ggt ttc ctt ggg tct 445
 Arg Glu Arg Gly Gly Glu Leu Leu Val His Thr Gly Phe Leu Gly Ser
 115 120 125
 tct cag gac cgt agt gcc tac cag acg att gac tca gca gag gcg ccc 493
 Ser Gln Asp Arg Ser Ala Tyr Gln Thr Ile Asp Ser Ala Glu Ala Pro
 130 135 140
 gca gat ccc ttt gca gtc cca gag ggc agg agt caa gat gcc cga ggg 541
 Ala Asp Pro Phe Ala Val Pro Glu Gly Arg Ser Gln Asp Ala Arg Gly
 145 150 155
 tac tgaagccagc cacgctgcgc ccggccctgc cccgggcctt cctcgtgcct gggagg 600
 Tyr

tcgttctagg gatgctcctg acctccgtct cttggacctg agatggaatg tgtccccagc 660
 tcagggattg cctgaaccaa gaggccagga gcccccatgg gccgcccagt accatgcaca 720
 ctctgtccc gaactccctg aggcctcccc tccttcagg gcacccactg gttcccaggc 780
 tggaaccagg gtctctcttt acctcctacc ccattggtggc accacagagg cctcagccg 840
 agtcctgcct gagtgttgca agctcaggcc tttaaggact gctgatgcc cctcaggcct 900
 cccccaagtt tgctgggctt tgggtggaagc cctgagagct tcaggctcctg ctcagcccca 960
 ggagcagttt ggcattgggag tgaggccccg tccttctcac tgcctggtca catggtgcct 1020
 agggatgcag ggctggaggc cagaggtgtc agcaacactg tgaccaccca caacctccag 1080
 cctccctttt cagagcacag cattaaagtt tggggaatto tgt 1123

<210> 121

<211> 636

<212> PRT

<213> Homo sapiens

<400> 121

Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu Gly Leu
 1 5 10 15
 Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu Asp Trp
 20 25 30
 Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly Leu Gln
 35 40 45

190/233

Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp Ile Phe
 50 55 60
 Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp Arg Asp
 65 70 75 80
 Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr Thr Tyr
 85 90 95
 Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp Phe Ser
 100 105 110
 Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu Ile Gly
 115 120 125
 Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu Met Asp
 130 135 140
 Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met Arg Leu
 145 150 155 160
 Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr Phe Asp
 165 170 175
 His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly Gly Pro
 180 185 190
 Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn Lys Asp
 195 200 205
 Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg Gly Ile
 210 215 220
 Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser Lys Gly
 225 230 235 240
 Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr His Glu
 245 250 255
 Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr Gln Pro
 260 265 270
 Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp Gly Gly
 275 280 285
 Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val Ser Ala
 290 295 300
 Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His Gly Gly
 305 310 315 320
 Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp Tyr Lys

191/233

	325		330		335
Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu Ala Gly					
340		345		350	
Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly Ser Ile					
355	360		365		
Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys Met Pro					
370	375		380		
Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp Ala Leu					
385	390		395		400
Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn Met Glu					
405	410		415		
Asn Leu Pro Val Asn Gly Gly Asn Gly Gln Ser Phe Gly Tyr Ile Leu					
420	425		430		
Tyr Glu Thr Ser Ile Thr Ser Ser Gly Ile Leu Ser Gly His Val His					
435	440		445		
Asp Arg Gly Gln Val Phe Val Asn Thr Val Ser Ile Gly Phe Leu Asp					
450	455		460		
Tyr Lys Thr Thr Lys Ile Ala Val Pro Leu Ile Gln Gly Tyr Thr Val					
465	470		475		480
Leu Arg Ile Leu Val Glu Asn Arg Gly Arg Val Asn Tyr Gly Glu Asn					
485	490		495		
Ile Asp Asp Gln Arg Lys Gly Leu Ile Gly Asn Leu Tyr Leu Asn Asp					
500	505		510		
Ser Pro Leu Lys Asn Phe Arg Ile Tyr Ser Leu Asp Met Lys Lys Ser					
515	520		525		
Phe Phe Gln Arg Phe Gly Leu Asp Lys Trp Ser Ser Leu Pro Glu Thr					
530	535		540		
Pro Thr Leu Pro Ala Phe Phe Leu Gly Ser Leu Ser Ile Ser Ser Thr					
545	550		555		560
Pro Cys Asp Thr Phe Leu Lys Leu Glu Gly Trp Glu Lys Gly Val Val					
565	570		575		
Phe Ile Asn Gly Gln Asn Leu Gly Arg Tyr Trp Asn Ile Gly Pro Gln					
580	585		590		
Lys Thr Leu Tyr Leu Pro Gly Pro Trp Leu Ser Ser Gly Ile Asn Gln					
595	600		605		

192/233

Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln Phe Thr

610

615

620

Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys

625

630

635

<210> 122

<211> 318

<212> PRT

<213> Homo sapiens

<400> 122

Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Leu Pro Phe Leu

1

5

10

15

Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser Gly Val

20

25

30

Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val Thr Gly

35

40

45

Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala Gln Arg

50

55

60

Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly Glu Leu

65

70

75

80

Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val Leu Val

85

90

95

Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe Ala Lys

100

105

110

Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn Asn Ala

115

120

125

Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe Glu Met

130

135

140

His Ile Gly Val Asn His Leu Gly His Phe Leu Leu Thr His Leu Leu

145

150

155

160

Leu Glu Lys Leu Lys Glu Ser Ala Pro Ser Arg Ile Val Asn Val Ser

165

170

175

Ser Leu Ala His His Leu Gly Arg Ile His Phe His Asn Leu Gln Gly

180

185

190

Glu Lys Phe Tyr Asn Ala Gly Leu Ala Tyr Cys His Ser Lys Leu Ala

193/233

195	200	205
Asn Ile Leu Phe Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly Ser Gly		
210	215	220
Val Thr Thr Tyr Ser Val His Pro Gly Thr Val Gln Ser Glu Leu Val		
225	230	235
Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser Phe Phe		
245	250	255
Ile Lys Thr Pro Gln Gln Gly Ala Gln Thr Ser Leu His Cys Ala Leu		
260	265	270
Thr Glu Gly Leu Glu Ile Leu Ser Gly Asn His Phe Ser Asp Cys His		
275	280	285
Val Ala Trp Val Ser Ala Gln Ala Arg Asn Glu Thr Ile Ala Arg Arg		
290	295	300
Leu Trp Asp Val Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp		
305	310	315

<210> 123

<211> 82

<212> PRT

<213> Homo sapiens

<400> 123

Met Ala Phe Thr Leu Tyr Ser Leu Leu Gln Ala Ala Leu Leu Cys Val
1 5 10 15
Asn Ala Ile Ala Val Leu His Glu Glu Arg Phe Leu Lys Asn Ile Gly
20 25 30
Trp Gly Thr Asp Gln Gly Ile Gly Gly Phe Gly Glu Glu Pro Gly Ile
35 40 45
Lys Ser Gln Leu Met Asn Leu Ile Arg Ser Val Arg Thr Val Met Arg
50 55 60
Val Pro Leu Ile Ile Val Asn Ser Ile Ala Ile Val Leu Leu Leu Leu
65 70 75 80
Phe Gly

<210> 124

194/233

<211> 247

<212> PRT

<213> Homo sapiens

<400> 124

Met His Leu Ala Arg Leu Val Gly Ser Cys Ser Leu Leu Leu Leu
 1 5 10 15
 Gly Ala Leu Ser Gly Trp Ala Ala Ser Asp Asp Pro Ile Glu Lys Val
 20 25 30
 Ile Glu Gly Ile Asn Arg Gly Leu Ser Asn Ala Glu Arg Glu Val Gly
 35 40 45
 Lys Ala Leu Asp Gly Ile Asn Ser Gly Ile Thr His Ala Gly Arg Glu
 50 55 60
 Val Glu Lys Val Phe Asn Gly Leu Ser Asn Met Gly Ser His Thr Gly
 65 70 75 80
 Lys Glu Leu Asp Lys Gly Val Gln Gly Leu Asn His Gly Met Asp Lys
 85 90 95
 Val Ala His Glu Ile Asn His Gly Ile Gly Gln Ala Gly Lys Glu Ala
 100 105 110
 Glu Lys Leu Gly His Gly Val Asn Asn Ala Ala Gly Gln Ala Gly Lys
 115 120 125
 Glu Ala Asp Lys Ala Val Gln Gly Phe His Thr Gly Val His Gln Ala
 130 135 140
 Gly Lys Glu Ala Glu Lys Leu Gly Gln Gly Val Asn His Ala Ala Asp
 145 150 155 160
 Gln Ala Gly Lys Glu Val Glu Lys Leu Gly Gln Gly Ala His His Ala
 165 170 175
 Ala Gly Gln Ala Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn
 180 185 190
 Gln Ala Ser Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser
 195 200 205
 Gly Ser Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser
 210 215 220
 Gly Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg
 225 230 235 240
 Ser Val Ala Asn Ile Met Pro

195/233

245

<210> 125

<211> 206

<212> PRT

<213> Homo sapiens

<400> 125

Met Ala Pro Ser His Leu Ser Val Arg Glu Met Arg Glu Asp Glu Lys

1 5 10 15

Pro Leu Val Leu Glu Met Leu Lys Ala Gly Val Lys Asp Thr Glu Asn

20 25 30

Arg Val Ala Leu His Ala Leu Thr Arg Pro Pro Ala Leu Leu Leu

35 40 45

Ala Ala Ala Ser Ser Gly Leu Arg Phe Val Leu Ala Ser Phe Ala Leu

50 55 60

Ala Leu Leu Leu Pro Val Phe Leu Ala Val Ala Ala Val Lys Leu Gly

65 70 75 80

Leu Arg Ala Arg Trp Gly Ser Leu Pro Pro Pro Gly Gly Leu Gly Gly

85 90 95

Pro Trp Val Ala Val Arg Gly Ser Gly Asp Val Cys Gly Val Leu Ala

100 105 110

Leu Ala Pro Gly Thr Asn Ala Gly Asp Gly Ala Arg Val Thr Arg Leu

115 120 125

Ser Val Ser Arg Trp His Arg Arg Arg Gly Val Gly Arg Arg Leu Leu

130 135 140

Ala Phe Ala Glu Ala Arg Ala Arg Ala Trp Ala Gly Gly Met Gly Glu

145 150 155 160

Pro Arg Ala Arg Leu Val Val Pro Val Ala Val Ala Ala Trp Gly Val

165 170 175

Gly Gly Met Leu Glu Gly Cys Gly Tyr Gln Ala Glu Gly Gly Trp Gly

180 185 190

Cys Leu Gly Tyr Thr Leu Val Arg Glu Phe Ser Lys Asp Leu

195 200 205

<210> 126

196/233

<211> 432

<212> PRT

<213> Homo sapiens

<400> 126

```

Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
  1             5             10             15
Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
          20             25             30
Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
          35             40             45
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
          50             55             60
Tyr Leu Glu Thr Gly Arg Gly Leu Cys Phe Pro Leu Val Lys Ala Cys
          65             70             75             80
Val Phe Gly Asn Glu Pro Lys Ala Ser Asp Glu Val Pro Leu Ala Pro
          85             90             95
Arg Thr Glu Ala Ala Glu Thr Thr Pro Met Trp Gln Ala Leu Lys Leu
          100            105            110
Leu Phe Cys Ala Thr Gly Leu Gln Val Ser Tyr Leu Thr Trp Gly Val
          115            120            125
Leu Gln Glu Arg Val Met Thr Arg Ser Tyr Gly Ala Thr Ala Thr Ser
          130            135            140
Pro Gly Glu Arg Phe Thr Asp Ser Gln Phe Leu Val Leu Met Asn Arg
          145            150            155            160
Val Leu Ala Leu Ile Val Ala Gly Leu Ser Cys Val Leu Cys Lys Gln
          165            170            175
Pro Arg His Gly Ala Pro Met Tyr Arg Tyr Ser Phe Ala Ser Leu Ser
          180            185            190
Asn Val Leu Ser Ser Trp Cys Gln Tyr Glu Ala Leu Lys Phe Val Ser
          195            200            205
Phe Pro Thr Gln Val Leu Ala Lys Ala Ser Lys Val Ile Pro Val Met
          210            215            220
Leu Met Gly Lys Leu Val Ser Arg Arg Ser Tyr Glu His Trp Glu Tyr
          225            230            235            240
Leu Thr Ala Thr Leu Ile Ser Ile Gly Val Ser Met Phe Leu Leu Ser

```


197/233

	245		250		255
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu					
	260		265		270
Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp					
	275		280		285
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe					
	290		295		300
Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu					
	305		310		315
Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu					
	325		330		335
Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln					
	340		345		350
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr					
	355		360		365
Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu					
	370		375		380
Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val					
	385		390		395
Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys					
	405		410		415
Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val					
	420		425		430

<210> 127

<211> 306

<212> PRT

<213> Homo sapiens

<400> 127

Met Gly His Arg Thr Leu Val Leu Pro Trp Val Leu Leu Thr Leu Cys			
1	5	10	15
Val Thr Ala Gly Thr Pro Glu Val Trp Val Gln Val Arg Met Glu Ala			
	20	25	30
Thr Glu Leu Ser Ser Phe Thr Ile Arg Cys Gly Phe Leu Gly Ser Gly			
	35	40	45

198/233

Ser Ile Ser Leu Val Thr Val Ser Trp Gly Gly Pro Asp Gly Ala Gly
 50 55 60
 Gly Thr Thr Leu Ala Val Leu His Pro Glu Arg Gly Ile Arg Gln Trp
 65 70 75 80
 Ala Pro Ala Arg Gln Ala Arg Trp Glu Thr Gln Ser Ser Ile Ser Leu
 85 90 95
 Ile Leu Glu Gly Ser Gly Ala Ser Ser Pro Cys Ala Asn Thr Thr Phe
 100 105 110
 Cys Cys Lys Phe Ala Ser Phe Pro Glu Gly Ser Trp Glu Ala Cys Gly
 115 120 125
 Ser Leu Pro Pro Ser Ser Asp Pro Gly Leu Ser Ala Pro Pro Thr Pro
 130 135 140
 Ala Pro Ile Leu Arg Ala Asp Leu Ala Gly Ile Leu Gly Val Ser Gly
 145 150 155 160
 Val Leu Leu Phe Gly Cys Val Tyr Leu Leu His Leu Leu Arg Arg His
 165 170 175
 Lys His Arg Pro Ala Pro Arg Leu Gln Pro Ser Arg Thr Ser Pro Gln
 180 185 190
 Ala Pro Arg Ala Arg Ala Trp Ala Pro Ser Gln Ala Ser Gln Ala Ala
 195 200 205
 Leu His Val Pro Tyr Ala Thr Ile Asn Thr Ser Cys Arg Pro Ala Thr
 210 215 220
 Leu Asp Thr Ala His Pro His Gly Gly Pro Ser Trp Trp Ala Ser Leu
 225 230 235 240
 Pro Thr His Ala Ala His Arg Pro Gln Gly Pro Ala Ala Trp Ala Ser
 245 250 255
 Thr Pro Ile Pro Ala Arg Gly Ser Phe Val Ser Val Glu Asn Gly Leu
 260 265 270
 Tyr Ala Gln Ala Gly Glu Arg Pro Pro His Thr Gly Pro Gly Leu Thr
 275 280 285
 Leu Phe Pro Asp Pro Arg Gly Pro Arg Ala Met Glu Gly Pro Leu Gly
 290 295 300
 Val Arg
 305

199/233

<210> 128

<211> 555

<212> PRT

<213> Homo sapiens

<400> 128

```

Met Gln Ser Cys Glu Ser Ser Gly Asp Ser Ala Asp Asp Pro Leu Ser
  1             5             10             15
Arg Gly Leu Arg Arg Arg Gly Gln Pro Arg Val Val Val Ile Gly Ala
      20             25             30
Gly Leu Ala Gly Leu Ala Ala Ala Lys Ala Leu Leu Glu Gln Gly Phe
      35             40             45
Thr Asp Val Thr Val Leu Glu Ala Ser Ser His Ile Gly Gly Arg Val
      50             55             60
Gln Ser Val Lys Leu Gly His Ala Thr Phe Glu Leu Gly Ala Thr Trp
      65             70             75             80
Ile His Gly Ser His Gly Asn Pro Ile Tyr His Leu Ala Glu Ala Asn
      85             90             95
Gly Leu Leu Glu Glu Thr Thr Asp Gly Glu Arg Ser Val Gly Arg Ile
      100            105            110
Ser Leu Tyr Ser Lys Asn Gly Val Ala Cys Tyr Leu Thr Asn His Gly
      115            120            125
Arg Arg Ile Pro Lys Asp Val Val Glu Glu Phe Ser Asp Leu Tyr Asn
      130            135            140
Glu Val Tyr Asn Leu Thr Gln Glu Phe Phe Arg His Asp Lys Pro Val
      145            150            155            160
Asn Ala Glu Ser Gln Asn Ser Val Gly Val Phe Thr Arg Glu Glu Val
      165            170            175
Arg Asn Arg Ile Arg Asn Asp Pro Asp Asp Pro Glu Ala Thr Lys Arg
      180            185            190
Leu Lys Leu Ala Met Ile Gln Gln Tyr Leu Lys Val Glu Ser Cys Glu
      195            200            205
Ser Ser Ser His Ser Met Asp Glu Val Ser Leu Ser Ala Phe Gly Glu
      210            215            220
Trp Thr Glu Ile Pro Gly Ala His His Ile Ile Pro Ser Gly Phe Met
      225            230            235            240

```

200/233

Arg Val Val Glu Leu Leu Ala Glu Gly Ile Pro Ala His Val Ile Gln
 245 250 255
 Leu Gly Lys Pro Val Arg Cys Ile His Trp Asp Gln Ala Ser Ala Arg
 260 265 270
 Pro Arg Gly Pro Glu Ile Glu Pro Arg Gly Glu Gly Asp His Asn His
 275 280 285
 Asp Thr Gly Glu Gly Gly Gln Gly Gly Glu Glu Pro Arg Gly Gly Arg
 290 295 300
 Trp Asp Glu Asp Glu Gln Trp Ser Val Val Val Glu Cys Glu Asp Cys
 305 310 315 320
 Glu Leu Ile Pro Ala Asp His Val Ile Val Thr Val Ser Leu Gly Val
 325 330 335
 Leu Lys Arg Gln Tyr Thr Ser Phe Phe Arg Pro Gly Leu Pro Thr Glu
 340 345 350
 Lys Val Ala Ala Ile His Arg Leu Gly Ile Gly Thr Thr Asp Lys Ile
 355 360 365
 Phe Leu Glu Phe Glu Glu Pro Phe Trp Gly Pro Glu Cys Asn Ser Leu
 370 375 380
 Gln Phe Val Trp Glu Asp Glu Ala Glu Ser His Thr Leu Thr Tyr Pro
 385 390 395 400
 Pro Glu Leu Trp Tyr Arg Lys Ile Cys Gly Phe Asp Val Leu Tyr Pro
 405 410 415
 Pro Glu Arg Tyr Gly His Val Leu Ser Gly Trp Ile Cys Gly Glu Glu
 420 425 430
 Ala Leu Val Met Glu Lys Cys Asp Asp Glu Ala Val Ala Glu Ile Cys
 435 440 445
 Thr Glu Met Leu Arg Gln Phe Thr Gly Asn Pro Asn Ile Pro Lys Pro
 450 455 460
 Arg Arg Ile Leu Arg Ser Ala Trp Gly Ser Asn Pro Tyr Phe Arg Gly
 465 470 475 480
 Ser Tyr Ser Tyr Thr Gln Val Gly Ser Ser Gly Ala Asp Val Glu Lys
 485 490 495
 Leu Ala Lys Pro Leu Pro Tyr Thr Glu Ser Ser Lys Thr Ala Pro Met
 500 505 510
 Gln Val Leu Phe Ser Gly Glu Ala Thr His Arg Lys Tyr Tyr Ser Thr

201/233

515 520 525
 Thr His Gly Ala Leu Leu Ser Gly Gln Arg Glu Ala Ala Arg Leu Ile
 530 535 540
 Glu Met Tyr Arg Asp Leu Phe Gln Gln Gly Thr
 545 550 555

<210> 129

<211> 250

<212> PRT

<213> Homo sapiens

<400> 129

Met Gly Ser Gln His Ser Ala Ala Ala Arg Pro Ser Ser Cys Arg Arg
 1 5 10 15
 Lys Gln Glu Asp Asp Arg Asp Gly Leu Leu Ala Glu Arg Glu Gln Glu
 20 25 30
 Glu Ala Ile Ala Gln Phe Pro Tyr Val Glu Phe Thr Gly Arg Asp Ser
 35 40 45
 Ile Thr Cys Leu Thr Cys Gln Gly Thr Gly Tyr Ile Pro Thr Glu Gln
 50 55 60
 Val Asn Glu Leu Val Ala Leu Ile Pro His Ser Asp Gln Arg Leu Arg
 65 70 75 80
 Pro Gln Arg Thr Lys Gln Tyr Val Leu Leu Ser Ile Leu Leu Cys Leu
 85 90 95
 Leu Ala Ser Gly Leu Val Val Phe Phe Leu Phe Pro His Ser Val Leu
 100 105 110
 Val Asp Asp Asp Gly Ile Lys Val Val Lys Val Thr Phe Asn Lys Gln
 115 120 125
 Asp Ser Leu Val Ile Leu Thr Ile Met Ala Thr Leu Lys Ile Arg Asn
 130 135 140
 Ser Asn Phe Tyr Thr Val Ala Val Thr Ser Leu Ser Ser Gln Ile Gln
 145 150 155 160
 Tyr Met Asn Thr Val Val Ser Thr Tyr Val Thr Thr Asn Val Ser Leu
 165 170 175
 Ile Pro Pro Arg Ser Glu Gln Leu Val Asn Phe Thr Gly Lys Ala Glu
 180 185 190

202/233

Met Gly Gly Pro Phe Ser Tyr Val Tyr Phe Phe Cys Thr Val Pro Glu
 195 200 205
 Ile Leu Val His Asn Ile Val Ile Phe Met Arg Thr Ser Val Lys Ile
 210 215 220
 Ser Tyr Ile Gly Leu Met Thr Gln Ser Ser Leu Glu Thr His His Tyr
 225 230 235 240
 Val Asp Cys Gly Gly Asn Ser Thr Ala Ile
 245 250

<210> 130

<211> 174

<212> PRT

<213> Homo sapiens

<400> 130

Met Gln Ala Pro Ala Phe Arg Asp Lys Lys Gln Gly Val Ser Ala Lys
 1 5 10 15
 Asn Gln Gly Ala His Asp Pro Asp Tyr Glu Asn Ile Thr Leu Ala Phe
 20 25 30
 Lys Asn Gln Asp His Ala Lys Gly Gly His Ser Arg Pro Thr Ser Gln
 35 40 45
 Val Pro Ala Gln Cys Arg Pro Pro Ser Asp Ser Thr Gln Val Pro Cys
 50 55 60
 Trp Leu Tyr Arg Ala Ile Leu Ser Leu Tyr Ile Leu Leu Ala Leu Ala
 65 70 75 80
 Phe Val Leu Cys Ile Ile Leu Ser Ala Phe Ile Met Val Lys Asn Ala
 85 90 95
 Glu Met Ser Lys Glu Leu Leu Gly Phe Lys Arg Glu Leu Trp Asn Val
 100 105 110
 Ser Asn Ser Val Gln Ala Cys Glu Glu Arg Gln Lys Arg Gly Trp Asp
 115 120 125
 Ser Val Gln Gln Ser Ile Thr Met Val Arg Ser Lys Ile Asp Arg Leu
 130 135 140
 Glu Thr Thr Leu Ala Gly Ile Lys Asn Ile Asp Thr Lys Val Gln Lys
 145 150 155 160
 Ile Leu Glu Val Leu Gln Lys Met Pro Gln Ser Ser Pro Gln

203/233

165

170

<210> 131

<211> 1908

<212> DNA

<213> Homo sapiens

<400> 131

atgaccacgt	ggagcctccg	gaggaggccg	gcccgcacgc	tgggactcct	gctgetggtc	60
gtcttgggct	tcctggtgct	tcgcaggetg	gactggagca	ccctgggtccc	tctgcggctc	120
cgccatcgac	agctggggct	gcaggccqag	ggctggaact	tcctgctgga	ggattccacc	180
ttctggatct	tcgggggctc	catccactat	ttccgtgtgc	ccagggagta	ctggagggac	240
cgcctgctga	agatgaaggc	ctgtggcttg	aacaccctca	ccacctatgt	tccgtggaac	300
ctgcatgagc	cagaaagagg	caaatttgac	ttctctggga	acctggacct	ggaggccttc	360
gtcctgatgg	ccgcagagat	cgggctgtgg	gtgattctgc	gtccaggccc	ctacatctgc	420
agtgagatgg	acctcggggg	cttgcccagc	tggctaactcc	aagaccctgg	catgaggctg	480
aggacaactt	acaagggett	caccgaagca	gtggaccttt	attttgacca	cctgatgtcc	540
agggtggtgc	cactccagta	caagcgtggg	ggacctatca	ttgccgtgca	ggtggagaat	600
gaatatgggt	cctataataa	agaccccgca	tacatgccct	acgtcaagaa	ggcactggag	660
gaccgtggca	ttgtggaact	gctcctgact	tcagacaaca	aggatgggct	gagcaagggg	720
attgtccagg	gagtcttggc	caccatcaac	ttgcagtcaa	cacacgagct	gcagctactg	780
accacctttc	tcttcaacgt	ccaggggact	cagcccaaga	tggatgatga	gtactggacg	840
gggtggtttg	actcgtgggg	aggccctcac	aatatcttgg	attctctctga	ggttttgaaa	900
accgtgtctg	ccattgtgga	cgcgggctcc	tccatcaacc	tctacatggt	ccacggaggc	960
accaactttg	gcttcatgaa	tggagccatg	cacttccatg	actacaagtc	agatgtcacc	1020
agctatgact	atgatgctgt	gctgacagaa	gccggcgatt	acacggccaa	gtacatgaag	1080
cttcgagaact	tcttcggctc	catctcaggc	atccctctcc	ctccccacc	tgaccttctt	1140
cccaagatgc	cgtatgagcc	cttaacgcca	gtcttgtacc	tgtctctgtg	ggacgccttc	1200
aagtacctgg	gggagccaat	caagtctgaa	aagcccatca	acatggagaa	cctgccagtc	1260
aatgggggaa	atggacagtc	cttcgggtac	attctctatg	agaccagcat	cacctcgtct	1320
ggcatcctca	gtggccacgt	gcatgatcgg	gggcagggtg	ttgtgaacac	agtatccata	1380
ggattcttgg	actacaagac	aacgaagatt	gctgtccccc	tgatccaggg	ttacaccgtg	1440
ctgaggatct	tgggtggagaa	tcgtgggcga	gtcaactatg	gggagaatat	tgatgaccag	1500
cgcaaaggct	taattggaaa	tctctatctg	aatgattcac	ccctgaaaaa	cttcagaatc	1560
tatagcctgg	atatgaagaa	gagcttcttt	cagaggttcg	gcctggacaa	atggagtccc	1620
ctcccagaaa	caccacatt	acctgctttc	ttcttgggta	gcttgtccat	cagctccacc	1680

204/233

ccttgtgaca cctttctgaa gctggagggc tgggagaagg gggttgtatt catcaatggc	1740
cagaaccttg gacgttactg gaacattgga ccccagaaga cgttttacct cccaggtccc	1800
tggttgagca gcggaatcaa ccaggtcatc gtttttgagg agacgatggc gggccctgca	1860
ttacagtcca cggaaacccc ccacctgggc aggaaccagt acattaag	1908

<210> 132

<211> 954

<212> DNA

<213> Homo sapiens

<400> 132

atgggtgagc tcatgttccc gctgttgetc ctcccttctgc ccttccttct gtatatgget	60
gcgccccaaa tcaggaaaat gctgtccagt ggggtgtgta catcaactgt tcagcttcct	120
gggaaagtag ttgtggtcac aggagctaat acaggtatcg ggaaggagac agccaaagag	180
ctggctcaga gaggagctcg agtatattta gcttgccggg atgtggaaaa gggggaattg	240
gtggccaaaag agatccagac cacgacaggg aaccagcagg tgttggtgcg gaaactggac	300
ctgtctgata ctaagtctat tcgagctttt gctaaggget tcttagctga ggaaaagcac	360
ctccacgttt tgatcaacaa tgcaggagtg atgatgtgtc cgtactcgaa gacagcagat	420
ggctttgaga tgcacatagg agtcaaccac ttgggtcact tcctcctaac ccactctgtg	480
ctagagaaac taaaggaatc agccccatca aggatagtaa atgtgtcttc cctcgcacat	540
cacctgggaa ggatccaact ccataacctg cagggcgaga aattctacaa tgcaggcctg	600
gcctactgtc acagcaagct agccaacatc ctcttcaccc aggaactggc ccggagacta	660
aaaggctctg gcgttacgac gtattctgta caccctggca cagtccaatc tgaactgggt	720
cggeactcat ctttcatgag atggatgtgg tggcttttct cttttttcat caagactcct	780
cagcagggag cccagaccag cctgcactgt gccttaacag aaggctctga gattctaagt	840
gggaatcatt tcagtgactg tcatgtggca tgggtctctg cccaagctcg taatgagact	900
atagcaaggc ggtgtggga cgtcagttgt gacctgctgg gcctcccaat agac	954

<210> 133

<211> 246

<212> DNA

<213> Homo sapiens

<400> 133

atggccttta ccctgtactc actgetgcag gcagccctgc tetgcgtcaa cgccatcgca	60
gtgetgcacg aggagcgatt cctcaagaac attggetggg gaacagacca ggggaattgg	120
ggatttgag aagagccggg aattaaatca cagctaataa acctatttcg atctgtaaga	180

205/233

accgtgatga gagtgccatt gataatagta aactcaattg caattgtgtt acttttatta 240
 tttgga 246

<210> 134

<211> 741

<212> DNA

<213> Homo sapiens

<400> 134

atgcatottg cacgtctggt cggctcctgc tccctccttc tgctactggg ggcctgtct 60
 ggatggggcg ccagcgatga cccattgag aaggctattg aagggatcaa ccgagggctg 120
 agcaatgcag agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 180
 gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag ccacaccggc 240
 aaggagtggg acaaaggcgt ccaggggctc aaccacggca tggacaagggt tgcccatgag 300
 atcaaccatg gtattggaca agcaggaaaag gaagcagaga agcttggcca tgggggtcaac 360
 aacgctgctg gacaggccgg gaaggaagca gacaaagcgg tccaagggtt ccacactggg 420
 gtccaccagg ctgggaagga agcagagaaa cttggccaag gggtaacca tgctgctgac 480
 caggctggaa aggaagtggg gaagcttggc caagggtgcc accatgctgc tggccaggcc 540
 ggggaaggagc tgcagaatgc tcataatggg gtcaaccaag ccagcaagga ggccaaccag 600
 ctgctgaatg gcaaccatca aagcggatct tccagccatc aaggaggggc cacaaccacg 660
 ccgttagcct ctggggcctc ggtcaacacg cctttcatca accttccgc cctgtggagg 720
 agcgtcgcca acatcatgcc c 741

<210> 135

<211> 618

<212> DNA

<213> Homo sapiens

<400> 135

atggccccc gccacctgtc agtgcgggag atgagggaa atgagaagcc cctgggtgctg 60
 gagatgctga aggcggcggt gaaggacacg gaaaaccgcg tggccctcca tgccttgaca 120
 cggcggcccg cctgtctcct cctggcgggc gccagcagcg gcctgcgctt tgctctggct 180
 tccttcgccc tggccctcct cctgccggtg ttcctggctg tggccgccc gaagetgggc 240
 ctgcggggcc gatggggctc gctgcctccg ccgggtggcc tggggggccc ctgggtggcc 300
 gtgcggggct ccgggtgacgt gtgtggggc ctggctctgg ccctggcac aaatgcaggg 360
 gacggggccc gggtaaccgc cctgtctgtc tctcgtggc accgccgcg gggcgtgggc 420
 aggaggtgc tggccttcgc ggaggcccg gctcgggcct gggctgggg catgggggag 480

206/233

ccccgggccc ggctcgtggt ccccggtggt gtggccgcct ggggggtggg agggatgctg 540
 gagggctgtg gctaccaggc cgaggggggc tggggctgcc tgggctacac gctgggtgag 600
 gaattcagca aagacctg 618

<210> 136

<211> 1296

<212> DNA

<213> Homo sapiens

<400> 136

atggacgcca gatggtgggc agtgggtggt ctggtgcgt tcccctccct aggggcaggt 60
 ggggagactc ccgaagcccc tccggagtca tggaccacgc tatggttctt ccgatttgtg 120
 gtgaatgctg ctggctatgc cagctttatg gtacctggt acctcctggt gcagtacttc 180
 aggcggaaga actacctgga gaccggtagg ggcctctgct ttcccctggt gaaagcttgt 240
 gtgtttggca atgagcccaa ggccctctgat gaggttcccc tggcgccccg aacagaggcg 300
 gcagagacca ccccgatgtg gcaggccctg aagctgctct tctgtgccac agggctccag 360
 gtgtcttata tgacttgggg tgtgctgcag gaaagagtga tgaccgcag ctatggggcc 420
 acagccacat caccgggtga gcgtttacg gactgcaggt tcctggtgct aatgaaccga 480
 gtgctggcac tgattgtggc tggcctctcc tgtgttctct gcaagcagcc ccggcatggg 540
 gcacccatgt accggtactc ctttgccagc ctgtccaatg tgetttagcag ctggtgccaa 600
 tacgaagctc ttaagttcgt cagcttcccc acccaggtgc tggccaaggc ctctaagggtg 660
 atccctgtca tgetgatggg aaagcttgtg tctcggcgca gctacgaaca ctgggagtac 720
 ctgacagcca cactcatctc cattgggggc agcatgttct tgctatccag cggaccagag 780
 ccccgagct cccagccac cacactctca ggccctcatct tactggcagg ttatattgct 840
 tttgacagct tcacctcaaa ctggcaggat gcctgtttg cctataagat gtcacgggtg 900
 cagatgatgt ttgggggtcaa tttcttctcc tgcctcttca cagtgggctc actgctagaa 960
 cagggggccc tactggaggg aaccgccttc atggggcgac acagtgagtt tgetgcccac 1020
 gccctgctac tctccatctg ctccgcatgt ggccagctct tcatctttta caccattggg 1080
 cagtttgggg ctgccgtctt caccatcate atgacctctc gccaggcctt tgccatcctt 1140
 ctttctctgcc ttctctatgg ccacactgtc actgtggtgg gagggctggg ggtggctgtg 1200
 gtctttgctg cctcctgct cagagtctac gcgcggggcc gtctaaagca acggggaaag 1260
 aaggctgtgc ctgttgagtc tcctgtgcag aaggtt 1296

<210> 137

<211> 918

<212> DNA

207/233

<213> Homo sapiens

<400> 137

atggggcacc	ggaccctggt	cctgccctgg	gtgctgctga	ccttggtgtgt	cactgcgggg	60
accccgagg	tgtgggttca	agttcggatg	gaggccaccg	agctctcgtc	cttcaccatc	120
cgttggtggg	tcctggggtc	tgggtccatc	tccttggtga	ctgtgagctg	ggggggcccc	180
gacggtgctg	gggggaccac	gctggctgtg	ttgcaccag	aacgtggcat	ccggcaatgg	240
gcccctgctc	gccaggcccg	ctgggaaacc	cagagcagca	tctctctcat	cctggaagge	300
tctggggcca	gcagcccctg	cgccaacacc	accttctgct	gcaagtttgc	gtccttccct	360
gagggctcct	gggaggcctg	tgggagcctc	ccgcccagct	cagaccaggg	gctctctgcc	420
ccgcccagctc	ctgcccccat	tctgcgggca	gacctggccg	ggatcttggg	ggtctcagga	480
gtcctcctct	ttggctgtgt	ctacctcctt	catctgctgc	gcgacataa	gcaccgccct	540
gcccctaggc	tccagccgtc	ccgcaccagc	ccccaggcac	cgagagcacg	agcatgggca	600
ccaagccagg	cctcccaggc	tgtcttccac	gtcccttatg	ccactatcaa	caccagctgc	660
cgcccagcta	ctttggacac	agctcaccac	catggggggc	cgtcctgggtg	ggcgtcactc	720
cccacccacg	ctgcacaccg	gccccagggc	cctgcccgcct	gggcctccac	acccatccct	780
gcacgtggca	gctttgtctc	tgttgagaat	ggactctacg	ctcaggcagg	ggagaggcct	840
cctcacactg	gtcccggcct	cactcttttc	cctgaccctc	ggggggcccag	ggccatggaa	900
ggacccttag	gagttcga					918

<210> 138

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 138

atgcaaagtt	gtgaatccag	tggtgacagt	gcggatgacc	ctctcagtcg	cggcctacgg	60
agaaggggac	agcctcgtgt	ggtggtgatc	ggcgccggct	tggctggcct	ggctgcagcc	120
aaagcacttc	ttgagcaggg	tttcacggat	gtcactgtgc	ttgaggcttc	cagccacatc	180
ggaggccgtg	tgcagagtgt	gaaacttgga	cacgccacct	ttgagctggg	agccacctgg	240
atccatgget	cccatgggaa	ccctatctat	catctagcag	aagccaacgg	cctcctggaa	300
gagacaaccg	atggggaacg	cagcgtgggc	cgcacagccc	tctattccaa	gaatggcgtg	360
gcctgctacc	ttaccaacca	cggccgcagg	atccccaagg	acgtggttga	ggaattcagc	420
gatttataca	acgaggtcta	taacttgacc	caggagttct	tccggcacga	taaaccagtc	480
aatgctgaaa	gtcaaaatag	cgtgggggtg	ttcaccgcag	aggaggtgcg	taaccgcctc	540
aggaatgacc	ctgacgaccc	agaggctacc	aagcgccctga	agctcgccat	gatccagcag	600
tacctgaagg	tggagagctg	tgagagcagc	tcacacagca	tggacgaggt	gtccctgagc	660

208/233

```

gccttcgggg agtggaccga gatccccggc getcaccaca tcatcccctc gggettcctg 720
cgggttgtgg agctgctggc ggagggcctc cctgcccacg tcatccagct agggaaacct 780
gtccgctgca ttcactggga ccaggcctca gcccgcctca gaggccctga gattgagccc 840
cgggggtgagg gcgaccacaa tcacgacact ggggaggggtg gccaggggtg agaggagccc 900
cgggggggca ggtgggatga ggatgagcag tggtcgggtg tggaggagtg cgaggactgt 960
gagctgatcc cggcggacca tgtgattgtg accgtgtcgc taggtgtgct aaagaggcag 1020
tacaccagtt tcttcgggcc aggcctgccc acagagaagg tggctgccat ccaccgctg 1080
ggcattggca ccaccgacaa gatctttctg gaattcgagg agcccttctg gggccctgag 1140
tgcaacagcc tacagtttgt gtgggaggac gaagcggaga gccacacct cactaccca 1200
cctgagctct ggtaccgcaa gatctgcggc tttgatgtcc tctaccgccc tgagcgctac 1260
ggccatgtgc tgagcggctg gatctgcggg gaggaggccc tggcatgga gaagtgtgat 1320
gacgaggcag tggccgagat ctgcacggag atgctgcgtc agttcacagg gaacccaac 1380
attccaaaac ctcggcgaat cttgcgtcgc gcctggggca gcaaccctta cttccgcggc 1440
tcctattcat acacgcaggt gggctccagc ggggcggatg tggagaagct ggccaagccc 1500
ctgccgtaca cggagagctc aaagacagcg cccatgcagg tgctgttttc cggtgaggcc 1560
accaccgca agtactattc caccaccac ggtgctctgc tgtccggcca gcgtgagget 1620
gcccgctca ttgagatgta ccgagacctc ttccagcagg ggacc 1665

```

<210> 139

<211> 750

<212> DNA

<213> Homo sapiens

<400> 139

```

atgggggtctc agcattccgc tgcgtctcgc cctcctcct gcaggcgaaa gcaagaagat 60
gacagggagc gtttgctggc tgaacgagag caggagaag ccattgctca gttcccatat 120
gtggaattca cggggagaga tagcatcacc tgtctcacgt gccaggggac aggtacatt 180
ccaacagagc aagtaaatga gttggtggct ttgatccac acagtgatca gagattgcgc 240
cctcagcgaa ctaagcaata tgtcctcctg tccatcctgc tttgtctcct ggcattctgg 300
ttggtgggtt tcttcctggt tccgcattca gtccttgtgg atgatgacgg catcaaagt 360
gtgaaagtca catttaataa gcaagactcc cttgtaattc tcaccatcat ggccaccctg 420
aaaatcagga actccaactt ctacacggtg gcagtgacca gcctgtccag ccagattcag 480
tacatgaaca cagtggtcag tacatatgtg actactaacg tctcccttat tccacctcgg 540
agtgagcaac tgggtgaattt taccgggaag gccgagatgg gaggaccgtt ttctatgtg 600
tacttctctt gcacgggtacc tgagatcctg gtgcacaaca tagtgatctt catgcgaact 660
tcagtgaaga ttccatacat tggcctcatg acccagagct cttgggagac acatcactat 720

```

209/233

gtggattgtg gaggaattc cacagctatt

750

<210> 140

<211> 522

<212> DNA

<213> Homo sapiens

<400> 140

atgcaagcac cagccttcag ggacaagaaa caggggggtct cagccaagaa tcaaggtgcc	60
catgacccag actatgagaa tatcaccttg gccttcaaaa atcaggacca tgcaaagggt	120
ggtcattcac gacccacgag ccaagtccca gcccagtga gcccgccctc agactccacc	180
cagggtccct gctggttgta cagagccatc ctgagcctgt acatcctcct gccctggcc	240
tttgtcctct gcatacctc gtcagccttc atcatggtga agaatgctga gatgtccaag	300
gagctgctgg gctttaaaag ggagctttgg aatgtctcaa actccgtaca agcatgcgaa	360
gagagacaga agagaggctg ggattccgtt cagcagagca tcaccatggt caggagcaag	420
attgatagat tagagacgac attagcaggc ataaaaaaca ttgacacaaa ggtacagaaa	480
atcttgagg tgctgcagaa aatgccacag tcctcacctc aa	522

<210> 141

<211> 3234

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (129)...(2039)

<400> 141

aatgagcgcc ggcgggcccgtg ttgccaggc gaccagcgcg cggtccgcc ccccgcgccg	60
aggtcccgcg gcgcggtga gtgcggactg gagtgggaac ccgggtcccc gcgcttagag	120
aacacgcg atg acc acg tgg agc ctc cgg cgg agg ccg gcc cgc acg ctg	170
Met Thr Thr Trp Ser Leu Arg Arg Arg Pro Ala Arg Thr Leu	
1 5 10	
gga ctc ctg ctg ctg gtc gtc ttg ggc ttc ctg gtg ctt cgc agg ctg	218
Gly Leu Leu Leu Leu Val Val Leu Gly Phe Leu Val Leu Arg Arg Leu	
15 20 25 30	
gac tgg agc acc ctg gtc cct ctg cgg ctc cgc cat cga cag ctg ggg	266
Asp Trp Ser Thr Leu Val Pro Leu Arg Leu Arg His Arg Gln Leu Gly	

210/233

35	40	45	
ctg cag gcc aag ggc tgg aac ttc atg ctg gag gat tcc acc ttc tgg			314
Leu Gln Ala Lys Gly Trp Asn Phe Met Leu Glu Asp Ser Thr Phe Trp			
50	55	60	
atc ttc ggg ggc tcc atc cac tat ttc cgt gtg ccc agg gag tac tgg			362
Ile Phe Gly Gly Ser Ile His Tyr Phe Arg Val Pro Arg Glu Tyr Trp			
65	70	75	
agg gac cgc ctg ctg aag atg aag gcc tgt ggc ttg aac acc ctc acc			410
Arg Asp Arg Leu Leu Lys Met Lys Ala Cys Gly Leu Asn Thr Leu Thr			
80	85	90	
acc tat gtt ccg tgg aac ctg cat gag cca gaa aga ggc aaa ttt gac			458
Thr Tyr Val Pro Trp Asn Leu His Glu Pro Glu Arg Gly Lys Phe Asp			
95	100	105	110
ttc tct ggg aac ctg gac ctg gag gcc ttc gtc ctg atg gcc gca gag			506
Phe Ser Gly Asn Leu Asp Leu Glu Ala Phe Val Leu Met Ala Ala Glu			
115	120	125	
atc ggg ctg tgg gtg att ctg cgt cca ggc ccc tac atc tgc agt gag			554
Ile Gly Leu Trp Val Ile Leu Arg Pro Gly Pro Tyr Ile Cys Ser Glu			
130	135	140	
atg gac ctc ggg ggc ttg ccc agc tgg cta ctc caa gac cct ggc atg			602
Met Asp Leu Gly Gly Leu Pro Ser Trp Leu Leu Gln Asp Pro Gly Met			
145	150	155	
agg ctg agg aca act tac aag ggc ttc acc gaa gca gtg gac ctt tat			650
Arg Leu Arg Thr Thr Tyr Lys Gly Phe Thr Glu Ala Val Asp Leu Tyr			
160	165	170	
ttt gac cac ctg atg tcc agg gtg gtg cca ctc cag tac aag cgt ggg			698
Phe Asp His Leu Met Ser Arg Val Val Pro Leu Gln Tyr Lys Arg Gly			
175	180	185	190
gga cct atc att gcc gtg cag gtg gag aat gaa tat ggt tcc tat aat			746
Gly Pro Ile Ile Ala Val Gln Val Glu Asn Glu Tyr Gly Ser Tyr Asn			
195	200	205	
aaa gac ccc gca tac atg ccc tac gtc aag aag gca ctg gag gac cgt			794
Lys Asp Pro Ala Tyr Met Pro Tyr Val Lys Lys Ala Leu Glu Asp Arg			
210	215	220	
ggc att gtg gaa ctg ctc ctg act tca gac aac aag gat ggg ctg agc			842

211/233

Gly Ile Val Glu Leu Leu Leu Thr Ser Asp Asn Lys Asp Gly Leu Ser	
225	230
aag ggg att gtc cag gga gtc ttg gcc acc atc aac ttg cag tca aca	890
Lys Gly Ile Val Gln Gly Val Leu Ala Thr Ile Asn Leu Gln Ser Thr	
240	245
cac gag ctg cag cta ctg acc acc ttt ctc ttc aac gtc cag ggg act	938
His Glu Leu Gln Leu Leu Thr Thr Phe Leu Phe Asn Val Gln Gly Thr	
255	260
cag ccc aag atg gtg atg gag tac tgg acg ggg tgg ttt gac tcg tgg	986
Gln Pro Lys Met Val Met Glu Tyr Trp Thr Gly Trp Phe Asp Ser Trp	
275	280
gga ggc cct cac aat atc ttg gat tct tct gag gtt ttg aaa acc gtg	1034
Gly Gly Pro His Asn Ile Leu Asp Ser Ser Glu Val Leu Lys Thr Val	
290	295
tct gcc att gtg gac gcc ggc tcc tcc atc aac ctc tac atg ttc cac	1082
Ser Ala Ile Val Asp Ala Gly Ser Ser Ile Asn Leu Tyr Met Phe His	
305	310
gga ggc acc aac ttt ggc ttc atg aat gga gcc atg cac ttc cat gac	1130
Gly Gly Thr Asn Phe Gly Phe Met Asn Gly Ala Met His Phe His Asp	
320	325
tac aag tca gat gtc acc agc tat gac tat gat gct gtg ctg aca gaa	1178
Tyr Lys Ser Asp Val Thr Ser Tyr Asp Tyr Asp Ala Val Leu Thr Glu	
335	340
gcc ggc gat tac acg gcc aag tac atg aag ctt cga gac ttc ttc ggc	1226
Ala Gly Asp Tyr Thr Ala Lys Tyr Met Lys Leu Arg Asp Phe Phe Gly	
355	360
tcc atc tca ggc atc cct ctc cct ccc cca cct gac ctt ctt ccc aag	1274
Ser Ile Ser Gly Ile Pro Leu Pro Pro Pro Pro Asp Leu Leu Pro Lys	
370	375
atg ccg tat gag ccc tta acg cca gtc ttg tac ctg tct ctg tgg gac	1322
Met Pro Tyr Glu Pro Leu Thr Pro Val Leu Tyr Leu Ser Leu Trp Asp	
385	390
gcc ctc aag tac ctg ggg gag cca atc aag tct gaa aag ccc atc aac	1370
Ala Leu Lys Tyr Leu Gly Glu Pro Ile Lys Ser Glu Lys Pro Ile Asn	
400	405
	410

213/233

595	600	605	
aac cag gtc atc gtt ttt gag gag acg atg gcg ggc cct gca tta cag			1994
Asn Gln Val Ile Val Phe Glu Glu Thr Met Ala Gly Pro Ala Leu Gln			
610	615	620	
ttc acg gaa acc ccc cac ctg ggc agg aac cag tac att aag tgag			2040
Phe Thr Glu Thr Pro His Leu Gly Arg Asn Gln Tyr Ile Lys			
625	630	635	
cggtggcacc ccctcctgct ggtgccagtg ggagactgcc gcctcctctt gacctgaagc			2100
ctggtggctg ctgccccacc cctcactgca aaagcatctc cttaagtagc aacctcaggg			2160
actgggggct acagtctgcc cctgtctcag ctcaaaaccc taagcctgca gggaaaggtg			2220
ggatggctct gggcctggct ttgttgatga tggctttcct acagccctgc tcttggtccg			2280
aggctgtcgg gctgtctcta ggggtgggagc agctaatacag atcgcccagc ctttggccct			2340
cagaaaaagt gctgaaacgt gcccttgcac cggacgtcac agccctgcca gcatctgctg			2400
gactcagggc tgetctttgc tggttcctgg gaggcttggc cacatccctc atggccccat			2460
tttatccccg aaatcctggg tgtgtcacca gtgtagaggg tggggaaggg gtgtctcacc			2520
tgagctgact ttgttcttcc ttcacaacct tctgagcctt ctttgggatt ctggaaggaa			2580
ctcggcgtga gaaacatgtg acttccccct tcccttccca ctcgctgctt cccacaggg			2640
gacaggetgg gctggagaaa cagaaatcct caccctgcgt cttcccaagt tagcaggtg			2700
ctctggtgtt cagtgaggag gacatgtgag tcctggcaga agccatggcc catgtctgca			2760
catccagggg ggaggacaga agggccagct cacatgtgag tcctggcaga agccatggcc			2820
catgtctgca catccagggg ggaggacaga agggccagct cacatgtgag tcctggcaga			2880
agccatggcc catgtctgca catccagggg ggaggacaga agggccagct cacatgtgag			2940
tcctggcaga agccatggcc catgtctgca catccagggg ggaggacaga agggccagct			3000
cacatgtgag tcctggcaga agccatggcc catgtctgca catccagggg ggaggacaga			3060
agggccagct cagtggcccc cggccccac cccccacgcc cgaacagcag gggcagagca			3120
gccctccttc gaagtgtgtc caagtccgca tttgagcctt gttctggggc ccagcccaac			3180
acctggcttg ggctcactgt cctgagttgc agtaaagcta taacctgaa tcac			3234

<210> 142

<211> 2490

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (70)...(1026)

214/233

<400> 142

```

agaaagagaa gccatagtcg gcgagcaacg ctggagcadc ccgctctggt gccgctgcag      60
ccggcagag atg gtt gag ctc atg ttc ccg ctg ttg ctc ctc ctt ctg ccc      111
      Met Val Glu Leu Met Phe Pro Leu Leu Leu Leu Leu Leu Pro
              1              5              10
ttc ctt ctg tat atg gct gcg ccc caa atc agg aaa atg ctg tcc agt      159
Phe Leu Leu Tyr Met Ala Ala Pro Gln Ile Arg Lys Met Leu Ser Ser
      15              20              25              30
ggg gtg tgt aca tca act gtt cag ctt cct ggg aaa gta gtt gtg gtc      207
Gly Val Cys Thr Ser Thr Val Gln Leu Pro Gly Lys Val Val Val Val
              35              40              45
aca gga gct aat aca ggt atc ggg aag gag aca gcc aaa gag ctg gct      255
Thr Gly Ala Asn Thr Gly Ile Gly Lys Glu Thr Ala Lys Glu Leu Ala
              50              55              60
cag aga gga gct cga gta tat tta gct tgc cgg gat gtg gaa aag ggg      303
Gln Arg Gly Ala Arg Val Tyr Leu Ala Cys Arg Asp Val Glu Lys Gly
              65              70              75
gaa ttg gtg gcc aaa gag atc cag acc acg aca ggg aac cag cag gtg      351
Glu Leu Val Ala Lys Glu Ile Gln Thr Thr Thr Gly Asn Gln Gln Val
              80              85              90
ttg gtg cgg aaa ctg gac ctg tct gat act aag tct att cga gct ttt      399
Leu Val Arg Lys Leu Asp Leu Ser Asp Thr Lys Ser Ile Arg Ala Phe
      95              100              105              110
gct aag ggc ttc tta gct gag gaa aag cac ctc cac gtt ttg atc aac      447
Ala Lys Gly Phe Leu Ala Glu Glu Lys His Leu His Val Leu Ile Asn
              115              120              125
aat gca gga gtg atg atg tgt ccg tac tcg aag aca gca gat ggc ttt      495
Asn Ala Gly Val Met Met Cys Pro Tyr Ser Lys Thr Ala Asp Gly Phe
              130              135              140
gag atg cac ata gga gtc aac cac ttg ggt cac ttc ctc cta acc cat      543
Glu Met His Ile Gly Val Asn His Leu Gly His Phe Leu Leu Thr His
              145              150              155
ctg ctg cta gag aaa cta aag gaa tca gcc cca tca agg ata gta aat      591
Leu Leu Leu Glu Lys Leu Lys Glu Ser Ala Pro Ser Arg Ile Val Asn
              160              165              170

```

gtg tct tcc ctc gca cat cac ctg gga agg atc cac ttc cat aac ctg	639
Val Ser Ser Leu Ala His His Leu Gly Arg Ile His Phe His Asn Leu	
175 180 185 190	
cag ggc gag aaa ttc tac aat gca ggc ctg gcc tac tgt cac agc aag	687
Gln Gly Glu Lys Phe Tyr Asn Ala Gly Leu Ala Tyr Cys His Ser Lys	
195 200 205	
cta gcc aac atc ctc ttc acc cag gaa ctg gcc cgg aga cta aaa ggc	735
Leu Ala Asn Ile Leu Phe Thr Gln Glu Leu Ala Arg Arg Leu Lys Gly	
210 215 220	
tct ggc gtt acg acg tat tct gta cac cct ggc aca gtc caa tct gaa	783
Ser Gly Val Thr Thr Tyr Ser Val His Pro Gly Thr Val Gln Ser Glu	
225 230 235	
ctg gtt cgg cac tca tct ttc atg aga tgg atg tgg tgg ctt ttc tcc	831
Leu Val Arg His Ser Ser Phe Met Arg Trp Met Trp Trp Leu Phe Ser	
240 245 250	
ttt ttc atc aag act cct cag cag gga gcc cag acc agc ctg cac tgt	879
Phe Phe Ile Lys Thr Pro Gln Gln Gly Ala Gln Thr Ser Leu His Cys	
255 260 265 270	
gcc tta aca gaa ggt ctt gag att cta agt ggg aat cat ttc agt gac	927
Ala Leu Thr Glu Gly Leu Glu Ile Leu Ser Gly Asn His Phe Ser Asp	
275 280 285	
tgt cat gtg gca tgg gtc tct gcc caa gct cgt aat gag act ata gca	975
Cys His Val Ala Trp Val Ser Ala Gln Ala Arg Asn Glu Thr Ile Ala	
290 295 300	
agg cgg ctg tgg gac gtc agt tgt gac ctg ctg ggc ctc cca ata gac	1023
Arg Arg Leu Trp Asp Val Ser Cys Asp Leu Leu Gly Leu Pro Ile Asp	
305 310 315	
taacagg cagtgccagt tggacccaag agaagactgc agcagactac acagtacttc	1080
ttgtcaaaat gattctcctt caagggttttc aaaaccttta gcacaaagag agcaaaacct	1140
tccagccttg cctgcttggt gtccagttaa aactcagtgt actgccagat togtctaaat	1200
gtctgtcatg tccagattta ctttgettct gttactgcca gagttactag agatatcata	1260
ataggataag aagaccctca tatgacctgc acagctcatt ttccttctga aagaaactac	1320
tacctaggag aatctaaget atagcagggg tgattttatgc aaatttgaac tagcttcttt	1380
gttcacaatt cagtctctcc caaccaacca gtcttcactt caagaggggc aactgcaac	1440
ctcagcttaa catgaataac aaaqactgqc tcaggagcaq qqcttgccca qqcatggtgq	1500

216/233

```

atcacccggag gtcagtagtt caagaccagc ctggccaaca tgggaaacc ccacctctac 1560
taaaaattgt gtatatcttt gtgtgtcttc ctgtttatgt gtgccaagg agtattttca 1620
caaagttcaa aacagccaca ataatcagag atggagcaaa ccagtgccat ccagtcttta 1680
tgcaaataaa atgctgcaaa gggaagcaga ttctgtatat gttggtaact acccaccaag 1740
agcacatggg tagcagggaa gaagtaaaaa aagagaagga gaatactgga agataatgca 1800
caaaatgaag ggactagtta aggattaact agccctttaa ggattaacta gttaaggatt 1860
aatagcaaaa gatattaaat atgctaacat agctatggag gaattgaggg caagcaccca 1920
ggactgatga ggtcttaaca aaaaccagtg tggcaaaaaa aaaaaaaaaa aaaaaaaaaa 1980
aaaaaaaaatc taaaaacaaa caaacaaaaa aaacaattct tcattcagaa aaattatctt 2040
agggaactgat attggttaatt atggtcaatt taataatatt ttggggcatt tccttacatt 2100
gtcttgacaa gattaaaatg tctgtgccaa aattttgtat tttatttgga gacttcttat 2160
caaaagtaat gctgccaag gaagtctaag gaattagtag tgttcccatc acttgtttg 2220
agtgtgctat tctaaaagat tttgatttcc tggaatgaca attatatatt aactttggtg 2280
ggggaaagag ttataggacc acagtcttca cttctgatac ttgtaaatta atcttttatt 2340
gcacttggtt tgaccattaa gctatatgtt tagaaatggt cattttacgg aaaaattaga 2400
aaaattctga taatagtga gaataaatga attaatgttt tacttaattt atattgaact 2460
gtcaatgaca aataaaaaatt ctttttgatt 2490

```

<210> 143

<211> 1465

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (84)...(332)

<400> 143

```

gaaggcgccg gccgtggagg cgccacgtcc cttgcggcgg cgggagagaa atcgettgga 60
cttcggggcg gcctcggacg gcc atg gcc ttt acc ctg tac tca ctg ctg 110

```

Met Ala Phe Thr Leu Tyr Ser Leu Leu

1

5

```

cag gca gcc ctg ctc tgc gtc aac gcc atc gca gtg ctg cac gag gag 158
Gln Ala Ala Leu Leu Cys Val Asn Ala Ile Ala Val Leu His Glu Glu
10 15 20 25
cga ttc ctc aag aac att ggc tgg gga aca gac cag gga att ggt gga 206
Arg Phe Leu Lys Asn Ile Gly Trp Gly Thr Asp Gln Gly Ile Gly Gly

```

217/233

30	35	40	
ttt gga gaa gag ccg gga att aaa tca cag cta atg aac ctt att cga			254
Phe Gly Glu Glu Pro Gly Ile Lys Ser Gln Leu Met Asn Leu Ile Arg			
45	50	55	
tct gta aga acc gtg atg aga gtg cca ttg ata ata gta aac tca att			302
Ser Val Arg Thr Val Met Arg Val Pro Leu Ile Ile Val Asn Ser Ile			
60	65	70	
gca att gtg tta ctt tta tta ttt gga tgaatatcag tggagaaaat g			350
Ala Ile Val Leu Leu Leu Leu Phe Gly			
75	80		
gagactcaga agaggacatg ccagtagaag ttattacttt ggtcattatt ggaatattta			410
tatcttagct ggctgacctt gcacttggtca aaaatgtaaa gctgaaaata aaaccagggt			470
ttctatttat ctgttttttt ttttaatggt gcacttgtag tttcattaca aaagatcaga			530
tcataaaagg cagtaactct ccaggactgg aatatctgat tgctcagtgt taatagtagt			590
tcatagtgtg gtgagattgt taaaagggtg caagactggt gcttctcttt ttttagatat			650
ttttctatct ctcaattctc agggatgaaa ttcttttttca aagttttgaa gttccttgca			710
acttagccat gatgtgagtg gttatcccta gataaaatta aaaggatttt taaaaagtaa			770
ttactgcaca taaaatgata aataggtaat ttgaataatt ttattttaag ctcttggtt			830
aattattttg tctattgtct cagctataaa ttcaaattta tacatactat tgagtattaa			890
tattctctga tttcaggagg aattctgtca gtcacatgat gattatgttt ttgtttaaca			950
ttctttccat gcacttgta ttttattaat ttgcctgaat gatgagacca gaccagtgtc			1010
tacagatttt cattgtcaga aaaatctata agtctgccct ttttacaatg atgatttaaa			1070
aaaaacaaca gcgtaaatat tagcccacaa gagcagtcct aaacaatcac aattacactg			1130
tactacccaa gaagactgtt tattgtgaag catttacctt tcaaaaaatc attacatttc			1190
tatttcttgg tggagcagca cattgtggag tgtgattctt aattcttcat tgagtttgtc			1250
aataggacat tgatgctgga taggttgtct tttgttttta tgtctcagac catcttgtga			1310
gattgtttgc ctatctcata atacagtttt atgcagaaag gttgaaacta tgtaaatggt			1370
ttttatggaa attatcagtt acaatatttt aaagggtgtag aatggcatct ttgtttatag			1430
gagaacattt gtaaataaag ttaaatttct aagtc			1465

<210> 144

<211> 917

<212> DNA

<213> Homo sapiens

<220>

218/233

<221> CDS

<222> (32)...(775)

<400> 144

tctctgcata cttcccgacc ttcccagcaa t atg cat ctt gca cgt ctg gtc	52
Met His Leu Ala Arg Leu Val	
1 5	
ggc tcc tgc tcc ctc ctt ctg cta ctg ggg gcc ctg tct gga tgg gcg	100
Gly Ser Cys Ser Leu Leu Leu Leu Leu Gly Ala Leu Ser Gly Trp Ala	
10 15 20	
gcc agc gat gac ccc att gag aag gtc att gaa ggg atc aac cga ggg	148
Ala Ser Asp Asp Pro Ile Glu Lys Val Ile Glu Gly Ile Asn Arg Gly	
25 30 35	
ctg agc aat gca gag aga gag gtg ggc aag gcc ctg gat ggc atc aac	196
Leu Ser Asn Ala Glu Arg Glu Val Gly Lys Ala Leu Asp Gly Ile Asn	
40 45 50 55	
agt gga atc acg cat gcc gga agg gaa gtg gag aag gtt ttc aac gga	244
Ser Gly Ile Thr His Ala Gly Arg Glu Val Glu Lys Val Phe Asn Gly	
60 65 70	
ctt agc aac atg ggg agc cac acc ggc aag gag ttg gac aaa ggc gtc	292
Leu Ser Asn Met Gly Ser His Thr Gly Lys Glu Leu Asp Lys Gly Val	
75 80 85	
cag ggg ctc aac cac ggc atg gac aag gtt gcc cat gag atc aac cat	340
Gln Gly Leu Asn His Gly Met Asp Lys Val Ala His Glu Ile Asn His	
90 95 100	
ggt att gga caa gca gga aag gaa gca gag aag ctt ggc cat ggg gtc	388
Gly Ile Gly Gln Ala Gly Lys Glu Ala Glu Lys Leu Gly His Gly Val	
105 110 115	
aac aac gct gct gga cag gcc ggg aag gaa gca gac aaa gcg gtc caa	436
Asn Asn Ala Ala Gly Gln Ala Gly Lys Glu Ala Asp Lys Ala Val Gln	
120 125 130 135	
ggg ttc cac act ggg gtc cac cag gct ggg aag gaa gca gag aaa ctt	484
Gly Phe His Thr Gly Val His Gln Ala Gly Lys Glu Ala Glu Lys Leu	
140 145 150	
ggc caa ggg gtc aac cat gct gct gac cag gct gga aag gaa gtg gag	532
Gly Gln Gly Val Asn His Ala Ala Asp Gln Ala Gly Lys Glu Val Glu	

219/233

155	160	165	
aag ctt ggc caa ggt gcc cac cat gct gct ggc cag gcc ggg aag gag			580
Lys Leu Gly Gln Gly Ala His His Ala Ala Gly Gln Ala Gly Lys Glu			
170	175	180	
ctg cag aat gct cat aat ggg gtc aac caa gcc agc aag gag gcc aac			628
Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser Lys Glu Ala Asn			
185	190	195	
cag ctg ctg aat ggc aac cat caa agc gga tct tcc agc cat caa gga			676
Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser Ser Ser His Gln Gly			
200	205	210	215
ggg gcc aca acc acg ccg tta gcc tct ggg gcc tcg gtc aac acg cct			724
Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly Ala Ser Val Asn Thr Pro			
220	225	230	
ttc atc aac ctt ccc gcc ctg tgg agg agc gtc gcc aac atc atg ccc			772
Phe Ile Asn Leu Pro Ala Leu Trp Arg Ser Val Ala Asn Ile Met Pro			
235	240	245	
taaactgg catccggcct tgctgggaga ataatgtcgc cgttgtcaca tcagctgaca			830
tgacctggag ggggtggggg tgggggacag gtttctgaaa tccctgaagg gggttgtact			890
gggatttgtg aataaacttg atacact			917

<210> 145

<211> 1306

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (74)...(694)

<400> 145

gaaggaccaa aggcgaccgg tgcaggtgca cgacgccagc tcccttctgg ggggccgggg	60
cctggggggtt gcc atg gcc ccc agc cac ctg tca gtg cgg gag atg agg	109
Met Ala Pro Ser His Leu Ser Val Arg Glu Met Arg	
1 5 10	
gaa gat gag aag ccc ctg gtg ctg gag atg ctg aag gcc ggc gtg aag	157
Glu Asp Glu Lys Pro Leu Val Leu Glu Met Leu Lys Ala Gly Val Lys	
15 20 25	

220/233

gac acg gaa aac cgc gtg gcc ctc cat gcc ttg aca cgg ccg ccg gcc	205
Asp Thr Glu Asn Arg Val Ala Leu His Ala Leu Thr Arg Pro Pro Ala	
30 35 40	
ctg ctc ctc ctg gcg gcg gcc agc agc ggc ctg cgc ttt gtc ctg gct	253
Leu Leu Leu Leu Ala Ala Ala Ser Ser Gly Leu Arg Phe Val Leu Ala	
45 50 55 60	
tcc ttc gcc ctg gcc ctc ctc ctg ccg gtg ttc ctg gct gtg gcc gcc	301
Ser Phe Ala Leu Ala Leu Leu Leu Pro Val Phe Leu Ala Val Ala Ala	
65 70 75	
gtg aag ctg ggc ctg cgg gcc cga tgg ggc tcg ctg cct ccg ccg ggt	349
Val Lys Leu Gly Leu Arg Ala Arg Trp Gly Ser Leu Pro Pro Pro Gly	
80 85 90	
ggc ctg ggg ggc ccc tgg gtg gcc gtg cgg ggc tcc ggt gac gtg tgt	397
Gly Leu Gly Gly Pro Trp Val Ala Val Arg Gly Ser Gly Asp Val Cys	
95 100 105	
ggg gtc ctg gct ctg gcc cct ggc aca aat gca ggg gac ggg gcc cgg	445
Gly Val Leu Ala Leu Ala Pro Gly Thr Asn Ala Gly Asp Gly Ala Arg	
110 115 120	
gtc acc cgc ctg tct gtc tct cgc tgg cac cgc cgc cgg ggc gtg ggc	493
Val Thr Arg Leu Ser Val Ser Arg Trp His Arg Arg Arg Gly Val Gly	
125 130 135 140	
agg agg ctg ctg gcc ttc gcg gag gcc cgg gct cgg gcc tgg gct ggg	541
Arg Arg Leu Leu Ala Phe Ala Glu Ala Arg Ala Arg Ala Trp Ala Gly	
145 150 155	
ggc atg ggg gag ccc cgg gcc cgg ctc gtg gtc ccc gtg gct gtg gcc	589
Gly Met Gly Glu Pro Arg Ala Arg Leu Val Val Pro Val Ala Val Ala	
160 165 170	
gcc tgg ggg gtg gga ggg atg ctg gag ggc tgt ggc tac cag gcc gag	637
Ala Trp Gly Val Gly Gly Met Leu Glu Gly Cys Gly Tyr Gln Ala Glu	
175 180 185	
ggg ggc tgg ggc tgc ctg ggc tac acg ctg gtg agg gaa ttc agc aaa	685
Gly Gly Trp Gly Cys Leu Gly Tyr Thr Leu Val Arg Glu Phe Ser Lys	
190 195 200	
gac ctg tgaagctaca gactgacagc cagggcaggg gaggagggag gggcgccag	740
Asp Leu	

221/233

205

```

cacctgatga tcgctactg tctgcgggtt cttttaacctg ctctccctca gtgagtcctc      800
aaccaccctg ggcccagaaa cagaggcctg ccgaggggag gagcctggcc tctgtccacc      860
cgtcagcagt gtgaagtctg ttgtgtttga gottctcaga gtggaatgac tccttttctt      920
tcctggccct cgggggcctc togaggtcag cctctccaac ccctacctca gtcctgtct      980
gcactgagaa acctccccgg gtgatgtctg caaagtctgt gctgtccgtg cccaggtg      1040
ggagagctat ctggggaggg ggagaggagg ccgagcagaa tacacccag agttaggggt      1100
tgcgactcgg cctccctggg acctggattg ggtcagatgc ctgtccttgg aggggacaag      1160
gttgactgt taggaggcgc gacgcacagg gctgccaggc ctggccctc tctgggaagg      1220
ttgagagctg agacgggcag cctgtccct tcctccagat ccgtctggtt ttttacaccg      1280
tttgtaata aagcctgaaa ccgctt                                           1306

```

<210> 146

<211> 2022

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (118)...(1416)

<400> 146

```

cttccgctgg ccgctggctc gctggccgct cctggaggcg gcggcgggag cgcagggggc      60
gcgcggcccc gggactcgca ttccccggtt cccctccac cccacgcggc ctggacc      117
atg gac gcc aga tgg tgg gca gtg gtg gtg ctg gct gcg ttc ccc tcc      165
Met Asp Ala Arg Trp Trp Ala Val Val Val Leu Ala Ala Phe Pro Ser
   1             5             10             15
cta ggg gca ggt ggg gag act ccc gaa gcc cct ccg gag tca tgg acc      213
Leu Gly Ala Gly Gly Glu Thr Pro Glu Ala Pro Pro Glu Ser Trp Thr
           20           25           30
cag cta tgg ttc ttc cga ttt gtg gtg aat gct gct ggc tat gcc agc      261
Gln Leu Trp Phe Phe Arg Phe Val Val Asn Ala Ala Gly Tyr Ala Ser
           35           40           45
ttt atg gta cct ggc tac ctc ctg gtg cag tac ttc agg cgg aag aac      309
Phe Met Val Pro Gly Tyr Leu Leu Val Gln Tyr Phe Arg Arg Lys Asn
           50           55           60
tac ctg gag acc ggt agg ggc ctc tgc ttt ccc ctg gtg aaa gct tgt      357

```

Tyr	Leu	Glu	Thr	Gly	Arg	Gly	Leu	Cys	Phe	Pro	Leu	Val	Lys	Ala	Cys	
65						70					75				80	
gtg	ttt	ggc	aat	gag	ccc	aag	gcc	tct	gat	gag	gtt	ccc	ctg	gcg	ccc	405
Val	Phe	Gly	Asn	Glu	Pro	Lys	Ala	Ser	Asp	Glu	Val	Pro	Leu	Ala	Pro	
				85					90					95		
cga	aca	gag	gcg	gca	gag	acc	acc	ccg	atg	tgg	cag	gcc	ctg	aag	ctg	453
Arg	Thr	Glu	Ala	Ala	Glu	Thr	Thr	Pro	Met	Trp	Gln	Ala	Leu	Lys	Leu	
			100					105					110			
ctc	ttc	tgt	gcc	aca	ggg	ctc	cag	gtg	tct	tat	ctg	act	tgg	ggg	gtg	501
Leu	Phe	Cys	Ala	Thr	Gly	Leu	Gln	Val	Ser	Tyr	Leu	Thr	Trp	Gly	Val	
		115				120					125					
ctg	cag	gaa	aga	gtg	atg	acc	cgc	agc	tat	ggg	gcc	aca	gcc	aca	tca	549
Leu	Gln	Glu	Arg	Val	Met	Thr	Arg	Ser	Tyr	Gly	Ala	Thr	Ala	Thr	Ser	
	130				135				140							
ccg	ggt	gag	cgc	ttt	acg	gac	tgc	cag	ttc	ctg	gtg	cta	atg	aac	cga	597
Pro	Gly	Glu	Arg	Phe	Thr	Asp	Ser	Gln	Phe	Leu	Val	Leu	Met	Asn	Arg	
145			150				155				160					
gtg	ctg	gca	ctg	att	gtg	gct	ggc	ctc	tcc	tgt	gtt	ctc	tgc	aag	cag	645
Val	Leu	Ala	Leu	Ile	Val	Ala	Gly	Leu	Ser	Cys	Val	Leu	Cys	Lys	Gln	
		165				170					175					
ccc	cgg	cat	ggg	gca	ccc	atg	tac	cgg	tac	tcc	ttt	gcc	agc	ctg	tcc	693
Pro	Arg	His	Gly	Ala	Pro	Met	Tyr	Arg	Tyr	Ser	Phe	Ala	Ser	Leu	Ser	
	180				185					190						
aat	gtg	ctt	agc	agc	tgg	tgc	caa	tac	gaa	gct	ctt	aag	ttc	gtc	agc	741
Asn	Val	Leu	Ser	Ser	Trp	Cys	Gln	Tyr	Glu	Ala	Leu	Lys	Phe	Val	Ser	
	195				200					205						
ttc	ccc	acc	cag	gtg	ctg	gcc	aag	gcc	tct	aag	gtg	atc	cct	gtc	atg	789
Phe	Pro	Thr	Gln	Val	Leu	Ala	Lys	Ala	Ser	Lys	Val	Ile	Pro	Val	Met	
	210				215				220							
ctg	atg	gga	aag	ctt	gtg	tct	cgg	cgc	agc	tac	gaa	cac	tgg	gag	tac	837
Leu	Met	Gly	Lys	Leu	Val	Ser	Arg	Arg	Ser	Tyr	Glu	His	Trp	Glu	Tyr	
225			230			235				240						
ctg	aca	gcc	aca	ctc	atc	tcc	att	ggg	gtc	agc	atg	ttt	ctg	cta	tcc	885
Leu	Thr	Ala	Thr	Leu	Ile	Ser	Ile	Gly	Val	Ser	Met	Phe	Leu	Leu	Ser	
	245				250					255						

223/233

agc gga cca gag ccc cgc agc tcc cca gcc acc aca ctc tca ggc ctc	933
Ser Gly Pro Glu Pro Arg Ser Ser Pro Ala Thr Thr Leu Ser Gly Leu	
260 265 270	
atc tta ctg gca ggt tat att gct ttt gac agc ttc acc tca aac tgg	981
Ile Leu Leu Ala Gly Tyr Ile Ala Phe Asp Ser Phe Thr Ser Asn Trp	
275 280 285	
cag gat gcc ctg ttt gcc tat aag atg tca tcg gtg cag atg atg ttt	1029
Gln Asp Ala Leu Phe Ala Tyr Lys Met Ser Ser Val Gln Met Met Phe	
290 295 300	
ggg gtc aat ttc ttc tcc tgc ctc ttc aca gtg ggc tca ctg cta gaa	1077
Gly Val Asn Phe Phe Ser Cys Leu Phe Thr Val Gly Ser Leu Leu Glu	
305 310 315 320	
cag ggg gcc cta ctg gag gga acc cgc ttc atg ggg cga cac agt gag	1125
Gln Gly Ala Leu Leu Glu Gly Thr Arg Phe Met Gly Arg His Ser Glu	
325 330 335	
ttt gct gcc cat gcc ctg cta ctc tcc atc tgc tcc gca tgt ggc cag	1173
Phe Ala Ala His Ala Leu Leu Leu Ser Ile Cys Ser Ala Cys Gly Gln	
340 345 350	
ctc ttc atc ttt tac acc att ggg cag ttt ggg gct gcc gtc ttc acc	1221
Leu Phe Ile Phe Tyr Thr Ile Gly Gln Phe Gly Ala Ala Val Phe Thr	
355 360 365	
atc atc atg acc ctc cgc cag gcc ttt gcc atc ctt ctt tcc tgc ctt	1269
Ile Ile Met Thr Leu Arg Gln Ala Phe Ala Ile Leu Leu Ser Cys Leu	
370 375 380	
ctc tat ggc cac act gtc act gtg gtg gga ggg ctg ggg gtg gct gtg	1317
Leu Tyr Gly His Thr Val Thr Val Val Gly Gly Leu Gly Val Ala Val	
385 390 395 400	
gtc ttt gct gcc ctc ctg ctc aga gtc tac gcg cgg ggc cgt cta aag	1365
Val Phe Ala Ala Leu Leu Leu Arg Val Tyr Ala Arg Gly Arg Leu Lys	
405 410 415	
caa cgg gga aag aag gct gtg cct gtt gag tct cct gtg cag aag gtt	1413
Gln Arg Gly Lys Lys Ala Val Pro Val Glu Ser Pro Val Gln Lys Val	
420 425 430	
tgaggggt ggaaagggcc tgaggggtga agtgaaatag gaccctccca ccacccctt	1470
ctgctgtaac ctctgagggga gctggctgaa agggcaaaat gcaggtgttt tctcagtatc	1530

224/233

```

acagaccagc tctgcagcag gggattgggg agcccaggag gcagccttcc cttttgcctt 1590
aagtcaccca tottccagta agcagtttat tctgagcccc gggggtagac agtcctcagt 1650
gagggggtttt ggggagtttg ggggtcaagag agcataggta ggttccacag ttactcttcc 1710
cacaagttcc cttaagtctt gccctagctg tgcctctgcc ccttccagac tcactccct 1770
ctgcaaatac ctgcatttct taccctgggt agaaaagcac aagcgggtgta ggctccaatg 1830
ctgctttccc aggaggggtga agatgggtgct gtgctgagga aaggggatgc agagccctgc 1890
ccagcaccac cacctctat gctcctggat ccctaggtc tgttccatga gcctgttgca 1950
ggttttggtta ctttagaaat gtaactttt gctcttataa ttttatttta ttaaattaaa 2010
ttactgcagt gg 2022

```

<210> 147

<211> 1227

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (75)...(995)

<400> 147

```

aaagacttcc tgcgatgaga acagagggcac aggtgccggc cctgcagccc ccagaacctg 60
gactgtaggg ggcc atg ggg cac cgg acc ctg gtc ctg ccc tgg gtg ctg 110
      Met Gly His Arg Thr Leu Val Leu Pro Trp Val Leu
           1             5             10
ctg acc ttg tgt gtc act gcg ggg acc ccg gag gtg tgg gtt caa gtt 158
Leu Thr Leu Cys Val Thr Ala Gly Thr Pro Glu Val Trp Val Gln Val
      15             20             25
cgg atg gag gcc acc gag ctc tcg tcc ttc acc atc cgt tgt ggg ttc 206
Arg Met Glu Ala Thr Glu Leu Ser Ser Phe Thr Ile Arg Cys Gly Phe
      30             35             40
ctg ggg tct ggc tcc atc tcc ctg gtg act gtg agc tgg ggg ggc ccc 254
Leu Gly Ser Gly Ser Ile Ser Leu Val Thr Val Ser Trp Gly Gly Pro
      45             50             55             60
gac ggt gct ggg ggg acc acg ctg gct gtg ttg cac cca gaa cgt ggc 302
Asp Gly Ala Gly Gly Thr Thr Leu Ala Val Leu His Pro Glu Arg Gly
      65             70             75
atc cgg caa tgg gcc cct gct cgc cag gcc cgc tgg gaa acc cag agc 350

```

225/233

Ile Arg Gln Trp Ala Pro Ala Arg Gln Ala Arg Trp Glu Thr Gln Ser	
80 85 90	
agc atc tct ctc atc ctg gaa ggc tct ggg gcc agc agc ccc tgc gcc	398
Ser Ile Ser Leu Ile Leu Glu Gly Ser Gly Ala Ser Ser Pro Cys Ala	
95 100 105	
aac acc acc ttc tgc tgc aag ttt gcg tcc ttc cct gag ggc tcc tgg	446
Asn Thr Thr Phe Cys Cys Lys Phe Ala Ser Phe Pro Glu Gly Ser Trp	
110 115 120	
gag gcc tgt ggg agc ctc ccg ccc agc tca gac cca ggg ctc tct gcc	494
Glu Ala Cys Gly Ser Leu Pro Pro Ser Ser Asp Pro Gly Leu Ser Ala	
125 130 135 140	
ccg ccg act cct gcc ccc att ctg cgg gca gac ctg gcc ggg atc ttg	542
Pro Pro Thr Pro Ala Pro Ile Leu Arg Ala Asp Leu Ala Gly Ile Leu	
145 150 155	
ggg gtc tca gga gtc ctc ctc ttt ggc tgt gtc tac ctc ctt cat ctg	590
Gly Val Ser Gly Val Leu Leu Phe Gly Cys Val Tyr Leu Leu His Leu	
160 165 170	
ctg cgc cga cat aag cac cgc cct gcc cct agg ctc cag ccg tcc cgc	638
Leu Arg Arg His Lys His Arg Pro Ala Pro Arg Leu Gln Pro Ser Arg	
175 180 185	
acc agc ccc cag gca ccg aga gca cga gca tgg gca cca agc cag gcc	686
Thr Ser Pro Gln Ala Pro Arg Ala Arg Ala Trp Ala Pro Ser Gln Ala	
190 195 200	
tcc cag gct gct ctt cac gtc cct tat gcc act atc aac acc agc tgc	734
Ser Gln Ala Ala Leu His Val Pro Tyr Ala Thr Ile Asn Thr Ser Cys	
205 210 215 220	
cgc cca gct act ttg gac aca gct cac ccc cat ggg ggg ccg tcc tgg	782
Arg Pro Ala Thr Leu Asp Thr Ala His Pro His Gly Gly Pro Ser Trp	
225 230 235	
tgg gcg tca ctc ccc acc cac gct gca cac cgg ccc cag ggc cct gcc	830
Trp Ala Ser Leu Pro Thr His Ala Ala His Arg Pro Gln Gly Pro Ala	
240 245 250	
gcc tgg gcc tcc aca ccc atc cct gca cgt ggc agc ttt gtc tct gtt	878
Ala Trp Ala Ser Thr Pro Ile Pro Ala Arg Gly Ser Phe Val Ser Val	
255 260 265	

226/233

gag aat gga ctc tac gct cag gca ggg gag agg cct cct cac act ggt 926
 Glu Asn Gly Leu Tyr Ala Gln Ala Gly Glu Arg Pro Pro His Thr Gly
 270 275 280
 ccc ggc ctc act ctt ttc cct gac cct cgg ggg ccc agg gcc atg gaa 974
 Pro Gly Leu Thr Leu Phe Pro Asp Pro Arg Gly Pro Arg Ala Met Glu
 285 290 295 300
 gga ccc tta gga gtt cga tgagagagac catgaggcca ctgggctt 1020
 Gly Pro Leu Gly Val Arg
 305
 tccccctccc aggcctcctg ggtgtcaccc ccttacttta attcttgggc ctccaataag 1080
 tgteccatag gtgtctggcc aggccacct gctgeggatg tggctctgtgt gcgtgtgtgg 1140
 gcacaggtgt gagtgtgtga gtgacagtta cccatttca gtcatttctt gctgcaacta 1200
 agtcagcaac acagttttctc tgatgtc 1227

<210> 148

<211> 2210

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (204)...(1871)

<400> 148

aggggacgcg agggcgagcg gggccccaca caggccgcgg cggtctggctc gggcccctac 60
 ggtcccggcg gcggctggag gaggaagcca ggcggctggc ggaggaggag agacggagga 120
 ggccgagacc ggagcgccgc tcgccgcaga cttacttccc cggtcagca gggaaagggt 180
 cctagaagggt gagecgggac ggt atg caa agt tgt gaa tcc agt ggt gac agt 233
 Met Gln Ser Cys Glu Ser Ser Gly Asp Ser
 1 5 10
 gcg gat gac cct ctc agt cgc ggc cta cgg aga agg gga cag cct cgt 281
 Ala Asp Asp Pro Leu Ser Arg Gly Leu Arg Arg Arg Gly Gln Pro Arg
 15 20 25
 gtg gtg gtg atc ggc gcc ggc ttg gct ggc ctg gct gca gcc aaa gca 329
 Val Val Val Ile Gly Ala Gly Leu Ala Gly Leu Ala Ala Ala Lys Ala
 30 35 40
 ctt ctt gag cag ggt ttc acg gat gtc act gtg ctt gag gct tcc agc 377

227/233

Leu Leu Glu Gln Gly Phe Thr Asp Val Thr Val Leu Glu Ala Ser Ser	
45 50 55	
cac atc gga ggc cgt gtg cag agt gtg aaa ctt gga cac gcc acc ttt	425
His Ile Gly Gly Arg Val Gln Ser Val Lys Leu Gly His Ala Thr Phe	
60 65 70	
gag ctg gga gcc acc tgg atc cat ggc tcc cat ggg aac cct atc tat	473
Glu Leu Gly Ala Thr Trp Ile His Gly Ser His Gly Asn Pro Ile Tyr	
75 80 85 90	
cat cta gca gaa gcc aac ggc ctc ctg gaa gag aca acc gat ggg gaa	521
His Leu Ala Glu Ala Asn Gly Leu Leu Glu Glu Thr Thr Asp Gly Glu	
95 100 105	
cgc agc gtg ggc cgc atc agc ctc tat tcc aag aat ggc gtg gcc tgc	569
Arg Ser Val Gly Arg Ile Ser Leu Tyr Ser Lys Asn Gly Val Ala Cys	
110 115 120	
tac ctt acc aac cac ggc cgc agg atc ccc aag gac gtg gtt gag gaa	617
Tyr Leu Thr Asn His Gly Arg Arg Ile Pro Lys Asp Val Val Glu Glu	
125 130 135	
ttc agc gat tta tac aac gag gtc tat aac ttg acc cag gag ttc ttc	665
Phe Ser Asp Leu Tyr Asn Glu Val Tyr Asn Leu Thr Gln Glu Phe Phe	
140 145 150	
cgg cac gat aaa cca gtc aat gct gaa agt caa aat agc gtg ggg gtg	713
Arg His Asp Lys Pro Val Asn Ala Glu Ser Gln Asn Ser Val Gly Val	
155 160 165 170	
ttc acc cga gag gag gtg cgt aac cgc atc agg aat gac cct gac gac	761
Phe Thr Arg Glu Glu Val Arg Asn Arg Ile Arg Asn Asp Pro Asp Asp	
175 180 185	
cca gag gct acc aag cgc ctg aag ctc gcc atg atc cag cag tac ctg	809
Pro Glu Ala Thr Lys Arg Leu Lys Leu Ala Met Ile Gln Gln Tyr Leu	
190 195 200	
aag gtg gag agc tgt gag agc agc tca cac agc atg gac gag gtg tcc	857
Lys Val Glu Ser Cys Glu Ser Ser Ser His Ser Met Asp Glu Val Ser	
205 210 215	
ctg agc gcc ttc ggg gag tgg acc gag atc ccc ggc gct cac cac atc	905
Leu Ser Ala Phe Gly Glu Trp Thr Glu Ile Pro Gly Ala His His Ile	
220 225 230	

atc	ccc	tgc	ggc	ttc	atg	cgg	gtt	gtg	gag	ctg	ctg	gcg	gag	ggc	atc	953
Ile	Pro	Ser	Gly	Phe	Met	Arg	Val	Val	Glu	Leu	Leu	Ala	Glu	Gly	Ile	
235					240				245						250	
cct	gcc	cac	gtc	atc	cag	cta	ggg	aaa	cct	gtc	cgc	tgc	att	cac	tgg	1001
Pro	Ala	His	Val	Ile	Gln	Leu	Gly	Lys	Pro	Val	Arg	Cys	Ile	His	Trp	
				255					260						265	
gac	cag	gcc	tca	gcc	cgc	ccc	aga	ggc	cct	gag	att	gag	ccc	cgg	ggc	1049
Asp	Gln	Ala	Ser	Ala	Arg	Pro	Arg	Gly	Pro	Glu	Ile	Glu	Pro	Arg	Gly	
				270					275						280	
gag	ggc	gac	cac	aat	cac	gac	act	ggg	gag	ggc	ggc	cag	ggc	gga	gag	1097
Glu	Gly	Asp	His	Asn	His	Asp	Thr	Gly	Glu	Gly	Gly	Gln	Gly	Gly	Glu	
				285					290						295	
gag	ccc	cgg	ggg	ggc	agg	tgg	gat	gag	gat	gag	cag	tgg	tgc	gtg	gtg	1145
Glu	Pro	Arg	Gly	Gly	Arg	Trp	Asp	Glu	Asp	Glu	Gln	Trp	Ser	Val	Val	
				300					305						310	
gtg	gag	tgc	gag	gac	tgt	gag	ctg	atc	ccg	gcg	gac	cat	gtg	att	gtg	1193
Val	Glu	Cys	Glu	Asp	Cys	Glu	Leu	Ile	Pro	Ala	Asp	His	Val	Ile	Val	
315					320					325					330	
acc	gtg	tgc	cta	ggc	gtg	cta	aag	agg	cag	tac	acc	agt	ttc	ttc	cgg	1241
Thr	Val	Ser	Leu	Gly	Val	Leu	Lys	Arg	Gln	Tyr	Thr	Ser	Phe	Phe	Arg	
				335					340						345	
cca	ggc	ctg	ccc	aca	gag	aag	gtg	gct	gcc	atc	cac	cgc	ctg	ggc	att	1289
Pro	Gly	Leu	Pro	Thr	Glu	Lys	Val	Ala	Ala	Ile	His	Arg	Leu	Gly	Ile	
				350					355						360	
ggc	acc	acc	gac	aag	atc	ttt	ctg	gaa	ttc	gag	gag	ccc	ttc	tgg	ggc	1337
Gly	Thr	Thr	Asp	Lys	Ile	Phe	Leu	Glu	Phe	Glu	Glu	Pro	Phe	Trp	Gly	
				365					370						375	
cct	gag	tgc	aac	agc	cta	cag	ttt	gtg	tgg	gag	gac	gaa	gcg	gag	agc	1385
Pro	Glu	Cys	Asn	Ser	Leu	Gln	Phe	Val	Trp	Glu	Asp	Glu	Ala	Glu	Ser	
				380					385						390	
cac	acc	ctc	acc	tac	cca	cct	gag	ctc	tgg	tac	cgc	aag	atc	tgc	ggc	1433
His	Thr	Leu	Thr	Tyr	Pro	Pro	Glu	Leu	Trp	Tyr	Arg	Lys	Ile	Cys	Gly	
395					400					405					410	
ttt	gat	gtc	ctc	tac	ccg	cct	gag	cgc	tac	ggc	cat	gtg	ctg	agc	ggc	1481
Phe	Asp	Val	Leu	Tyr	Pro	Pro	Glu	Arg	Tyr	Gly	His	Val	Leu	Ser	Gly	

229/233

415	420	425	
tgg atc tgc ggg gag gag gcc ctc gtc atg gag aag tgt gat gac gag			1529
Trp Ile Cys Gly Glu Glu Ala Leu Val Met Glu Lys Cys Asp Asp Glu			
430	435	440	
gca gtg gcc gag atc tgc acg gag atg ctg cgt cag ttc aca ggg aac			1577
Ala Val Ala Glu Ile Cys Thr Glu Met Leu Arg Gln Phe Thr Gly Asn			
445	450	455	
ccc aac att cca aaa cct cgg cga atc ttg cgc tcg gcc tgg ggc agc			1625
Pro Asn Ile Pro Lys Pro Arg Arg Ile Leu Arg Ser Ala Trp Gly Ser			
460	465	470	
aac cct tac ttc cgc ggc tcc tat tca tac acg cag gtg ggc tcc agc			1673
Asn Pro Tyr Phe Arg Gly Ser Tyr Ser Tyr Thr Gln Val Gly Ser Ser			
475	480	485	490
ggg gcg gat gtg gag aag ctg gcc aag ccc ctg ccg tac acg gag agc			1721
Gly Ala Asp Val Glu Lys Leu Ala Lys Pro Leu Pro Tyr Thr Glu Ser			
495	500	505	
tca aag aca gcg ccc atg cag gtg ctg ttt tcc ggt gag gcc acc cac			1769
Ser Lys Thr Ala Pro Met Gln Val Leu Phe Ser Gly Glu Ala Thr His			
510	515	520	
cgc aag tac tat tcc acc acc cac ggt gct ctg ctg tcc ggc cag cgt			1817
Arg Lys Tyr Tyr Ser Thr Thr His Gly Ala Leu Leu Ser Gly Gln Arg			
525	530	535	
gag gct gcc cgc ctc att gag atg tac cga gac ctc ttc cag cag ggg			1865
Glu Ala Ala Arg Leu Ile Glu Met Tyr Arg Asp Leu Phe Gln Gln Gly			
540	545	550	
acc tgagggctgt cctcgtctgt gagaagagcc actaactcgt gacctccagc ct			1920
Thr			
555			
gccccttctgt gccgtgtgct cctgccttcc tgatcctctg tagaaaggat ttttatcttc			1980
tgtagagcta gccgccctga ctgccttcag acctggccct gtagcttttc tttttctcca			2040
ggctgggccc tgagcaggtg ggccgttgag ttacctctgt gctggatccc gtgccccac			2100
ttgcctaccc totgtcctgc cttgtttattg taagtgcctt caatactttg cattttggga			2160
taataaaaaa ggctccctcc cctgcccctc agcttctctc tggttttctc			2210

<210> 149

230/233

<211> 1493

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (93)...(845)

<400> 149

```

ctcaagctgg caggtggctg ggggagcggc cggagaggag ctgccgggag ttcgtgccct      60
gcaggacatg acaccagtgg catatcacgg cc atg ggg tct cag cat tcc gct      113
                               Met Gly Ser Gln His Ser Ala
                               1             5

gct gct cgc ccc tcc tcc tgc agg cga aag caa gaa gat gac agg gac      161
Ala Ala Arg Pro Ser Ser Cys Arg Arg Lys Gln Glu Asp Asp Arg Asp
      10             15             20

ggg ttg ctg gct gaa cga gag cag gaa gaa gcc att gct cag ttc cca      209
Gly Leu Leu Ala Glu Arg Glu Gln Glu Glu Ala Ile Ala Gln Phe Pro
      25             30             35

tat gtg gaa ttc acc ggg aga gat agc atc acc tgt ctc acg tgc cag      257
Tyr Val Glu Phe Thr Gly Arg Asp Ser Ile Thr Cys Leu Thr Cys Gln
      40             45             50             55

ggg aca ggc tac att cca aca gag caa gta aat gag ttg gtg gct ttg      305
Gly Thr Gly Tyr Ile Pro Thr Glu Gln Val Asn Glu Leu Val Ala Leu
      60             65             70

atc cca cac agt gat cag aga ttg cgc cct cag cga act aag caa tat      353
Ile Pro His Ser Asp Gln Arg Leu Arg Pro Gln Arg Thr Lys Gln Tyr
      75             80             85

gtc ctc ctg tcc atc ctg ctt tgt ctc ctg gca tct ggt ttg gtg gtt      401
Val Leu Leu Ser Ile Leu Leu Cys Leu Leu Ala Ser Gly Leu Val Val
      90             95             100

ttc ttc ctg ttt ccg cat tca gtc ctt gtg gat gat gac ggc atc aaa      449
Phe Phe Leu Phe Pro His Ser Val Leu Val Asp Asp Asp Gly Ile Lys
      105             110             115

gtg gtg aaa gtc aca ttt aat aag caa gac tcc ctt gta att ctc acc      497
Val Val Lys Val Thr Phe Asn Lys Gln Asp Ser Leu Val Ile Leu Thr
      120             125             130             135

```

231/233

atc atg gcc acc ctg aaa atc agg aac tcc aac ttc tac acg gtg gca	545
Ile Met Ala Thr Leu Lys Ile Arg Asn Ser Asn Phe Tyr Thr Val Ala	
140 145 150	
gtg acc agc ctg tcc agc cag att cag tac atg aac aca gtg gtc agt	593
Val Thr Ser Leu Ser Ser Gln Ile Gln Tyr Met Asn Thr Val Val Ser	
155 160 165	
aca tat gtg act act aac gtc tcc ctt att cca cct cgg agt gag caa	641
Thr Tyr Val Thr Thr Asn Val Ser Leu Ile Pro Pro Arg Ser Glu Gln	
170 175 180	
ctg gtg aat ttt acc ggg aag gcc gag atg gga gga ccg ttt tcc tat	689
Leu Val Asn Phe Thr Gly Lys Ala Glu Met Gly Gly Pro Phe Ser Tyr	
185 190 195	
gtg tac ttc ttc tgc acg gta cct gag atc ctg gtg cac aac ata gtg	737
Val Tyr Phe Phe Cys Thr Val Pro Glu Ile Leu Val His Asn Ile Val	
200 205 210 215	
atc ttc atg cga act tca gtg aag att tca tac att ggc ctc atg acc	785
Ile Phe Met Arg Thr Ser Val Lys Ile Ser Tyr Ile Gly Leu Met Thr	
220 225 230	
cag agc tcc ttg gag aca cat cac tat gtg gat tgt gga gga aat tcc	833
Gln Ser Ser Leu Glu Thr His His Tyr Val Asp Cys Gly Gly Asn Ser	
235 240 245	
aca gct att taacaactgc tattggttct tccacacagc gcctgtagaa gagagcac	890
Thr Ala Ile	
250	
agcatatggt cccaaggcct gagttctgga cctaccccca cgtggtgtaa gcagaggagg	950
aattggttca cttaactccc agcaaacatc ctctgccac ttaggaggaa acacctccct	1010
atggtaccat ttatgtttct cagaaccagc agaatcagtg cctagcctgt gccagcaaa	1070
tagttggcac tcaataaaga tttgcagaat ttaatacaga tcttttcagc tgttcttagg	1130
gcattataaa tggaaatcat aacgtggttc taggttatca aaccatggag tgatgtggag	1190
ctaggattgt gagtgacctg caggccatta tcagtgcctc atctgtgcag aagtcgcagc	1250
agagagggac catccaaata cctaagagaa aacagacctc gtcaggatat gaatttgttt	1310
cagctgttcc caaaggcctg ggagcttttt gaaaagaaag aaaaaagtgt gttggttttt	1370
ttttttttta gaaagttaga attgttttta ccaagagtct atgtggggct tgattcaccc	1430
ttcatccatt ggetggaaca tggattgggg atttgataga aaaataaacc ctgcttttga	1490
ttc	1493

232/233

<210> 150
 <211> 1264
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> CDS
 <222> (26)...(550)
 <400> 150

```

aatctacaag caccaggaag tcaag atg caa gca cca gcc ttc agg gac aag      52
                                Met Gln Ala Pro Ala Phe Arg Asp Lys
                                1              5

aaa cag ggg gtc tca gcc aag aat caa ggt gcc cat gac cca gac tat      100
Lys Gln Gly Val Ser Ala Lys Asn Gln Gly Ala His Asp Pro Asp Tyr
  10              15              20              25

gag aat atc acc ttg gcc ttc aaa aat cag gac cat gca aag ggt ggt      148
Glu Asn Ile Thr Leu Ala Phe Lys Asn Gln Asp His Ala Lys Gly Gly
          30              35              40

cat tca cga ccc acg agc caa gtc cca gcc cag tgc agg ccg ccc tca      196
His Ser Arg Pro Thr Ser Gln Val Pro Ala Gln Cys Arg Pro Pro Ser
          45              50              55

gac tcc acc cag gtc ccc tgc tgg ttg tac aga gcc atc ctg agc ctg      244
Asp Ser Thr Gln Val Pro Cys Trp Leu Tyr Arg Ala Ile Leu Ser Leu
          60              65              70

tac atc ctc ctg gcc ctg gcc ttt gtc ctc tgc atc atc ctg tca gcc      292
Tyr Ile Leu Leu Ala Leu Ala Phe Val Leu Cys Ile Ile Leu Ser Ala
          75              80              85

ttc atc atg gtg aag aat gct gag atg tcc aag gag ctg ctg ggc ttt      340
Phe Ile Met Val Lys Asn Ala Glu Met Ser Lys Glu Leu Leu Gly Phe
          90              95              100              105

aaa agg gag ctt tgg aat gtc tca aac tcc gta caa gca tgc gaa gag      388
Lys Arg Glu Leu Trp Asn Val Ser Asn Ser Val Gln Ala Cys Glu Glu
          110              115              120

aga cag aag aga ggc tgg gat tcc gtt cag cag agc atc acc atg gtc      436
Arg Gln Lys Arg Gly Trp Asp Ser Val Gln Gln Ser Ile Thr Met Val

```

233/233

125	130	135	
agg agc aag att gat aga tta gag acg aca tta gca ggc ata aaa aac			484
Arg Ser Lys Ile Asp Arg Leu Glu Thr Thr Leu Ala Gly Ile Lys Asn			
140	145	150	
att gac aca aag gta cag aaa atc ttg gag gtg ctg cag aaa atg cca			532
Ile Asp Thr Lys Val Gln Lys Ile Leu Glu Val Leu Gln Lys Met Pro			
155	160	165	
cag tcc tca cct caa taaatgagag gacattgtgg cagccaaagc cac			580
Gln Ser Ser Pro Gln			
170			
aacttggaag atggggctgc acctgccaac gaagacggga aatgaccccc cccccagcc			640
tagtgtgaac ctgcccctcg tcccacgtat agaaaaacct cgagtcattg tgaatgagtg			700
tctcgagatt gtcgtgtgt gtgtacacct gcgtgcgtgt gtgtgcgtgt gtgcgcgtgt			760
gttcgtgtat gtgcgtgtgt gcgtgcgcgt gtgtgtgcat ttgcaaagg gtggacattt			820
cagtgtatct ccagaaagg tgatgaatga ataggactga gagtcacagt gaatgtggca			880
tgcattgctg tgatcatgtga catatgtgag tctcgccatg tcacgggtgg tggtgtgtc			940
tgagcacctc cagcagatgt cactctgagt gtgggtgttg gtgacatgca ttgcacgggc			1000
ctgtctccct gtttgtgtaa acatactaga gtatactgcg gcgtgttttc tgtctaccca			1060
tgtcatggtg ggggagattt atctccgtac atgtgggtgt cgcattgtgt gccctgtcac			1120
tatctgtggc tgggtgaacg gctgtgtcat tatgagtgtg ccgagttatg ccacctgtg			1180
tgctcagggc acatgcacac agacatttat ctctgcactc acattttgtg acttatgaag			1240
ataaataaag tcaagggaaa acag			1264